

| Result No. | Query |       |        | ID | Description |
|------------|-------|-------|--------|----|-------------|
|            | Score | Match | Length |    |             |
| 1          | 643   | 92.3  | 137    | 2  | JC1241      |
| 2          | 464   | 66.6  | 132    | 2  | S17182      |
| 3          | 449   | 64.4  | 133    | 2  | S17183      |
| 4          | 387   | 55.5  | 125    | 2  | AJ1454      |
| 5          | 83.5  | 12.0  | 698    | 1  | S00742      |
| 6          | 83    | 11.9  | 722    | 2  | AF1421      |
| 7          | 80    | 11.5  | 645    | 1  | OEPP1       |
| 8          | 80    | 11.5  | 645    | 1  | S07751      |
| 9          | 76.5  | 11.0  | 306    | 2  | T9067       |
| 10         | 75    | 10.8  | 1810   | 2  | T31092      |
| 11         | 73.5  | 10.5  | 412    | 2  | A70839      |
| 12         | 72.5  | 10.4  | 84     | 2  | S75757      |
| 13         | 72    | 10.3  | 254    | 2  | S40702      |
| 14         | 72    | 10.3  | 449    | 2  | H97249      |
| 15         | 72    | 10.3  | 616    | 2  | F90371      |
| 16         | 71.5  | 10.3  | 293    | 2  | D70514      |
| 17         | 71.5  | 10.3  | 722    | 2  | AD1796      |
| 18         | 70.5  | 10.1  | 842    | 2  | T04880      |
| 19         | 70    | 10.0  | 389    | 1  | S73933      |
| 20         | 70    | 10.0  | 537    | 2  | G82873      |
| 21         | 70    | 10.0  | 1147   | 2  | A82340      |
| 22         | 69.5  | 10.0  | 182    | 2  | F88979      |
| 23         | 69.5  | 10.0  | 746    | 2  | G02838      |
| 24         | 69    | 9.9   | 408    | 2  | B64708      |
| 25         | 68.5  | 9.8   | 464    | 2  | C69356      |
| 26         | 68.5  | 9.8   | 467    | 1  | B44038      |
| 27         | 68.5  | 9.8   | 574    | 2  | T41068      |
| 28         | 68    | 9.8   | 448    | 1  | S24756      |
| 29         | 67.5  | 9.7   | 352    | 2  | H87236      |

100% Local Samplarity 99.00; Acc: 99.00; 127  
 Matches 88; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

```
QY 1 MNHTSQAFITAAAGGPPNYERIKEEYEVAEMGAPHGASASVRTTVINMPREVSPDPHVW 60
Db 1 MSHTVQTFSPVNSGQPPNYEMLKEEBEVAVLGGPHNPAPPTSTVIHIRSTVSPDPHVW 60
QY 61 SLFNTLPMNFCCLGFTAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVVI 120
Db 61 SLFNTLPMNFCCLGFTAFAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNIWALILGILMTIL 120
QY 121 TIVSVIII 128
Db 121 LIVIPVLI 128
RESULT 3
S17183
interferon-induced protein 1-8D - human
C:Species: Homo sapiens (man)
C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C:Accession: S17183
R:Lewin, A.R.; Reid, L.B.; McMahon, M.; Stark, G.R.; Kerr, I.M.
Eur. J. Biochem. 199, 417-423, 1991
A:Title: Molecular analysis of a human interferon-inducible gene family.
A:Reference number: S17182; MUID:91301153; PMID:1906403
A:Accession: S17183
A:Molecule type: DNA
A:Residues: 1-132 <LEW>
A:CROSS-references: UNIPROT:Q01629; EMBL:X57351; NID:g311373; PIDN:CAA40625.1; PID:g22339
Query Match 64.4%; Score 449; DB 2; Length 132;
Best Local Similarity 65.4%; Pred. No. 3.6e-40;
Matches 8; Conservative 17; Mismatches 27; Indels 2; Gaps 2;
QY 1 MNHTSQAFITAAAGGPPNYERIKEEYEVAEMGAPHGASASVRTTVINMPREVSPDPHVW 60
Db 1 MNHIVQTF-SPVNSGQPPNYEMLKEEQEVAVLGGPHNPAPPTSTVIHIRSTVSPDPHVW 59
QY 61 SLFNTLPMNFCCLGFTAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVVI 120
Db 60 SLFNTLPMNFCCLGFTAFAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNIWALILGIFMTIL 119
QY 121 TIVSVIIIVLNAQ 133
Db 120 LVI-IPVLVVQAQ 131
RESULT 4
A31454
interferon-inducible protein - human (clone 9-27)
C:Species: Homo sapiens (man)
C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 09-Jul-2004
C:Accession: A31454
R:Reid, L.E.; Brasnett, A.H.; Gilbert, C.S.; Porter, A.C.G.; Gewert, D.R.; Stark, G.R.;
Proc. Natl. Acad. Sci. U.S.A. 86, 840-844, 1989
A:Title: A single DNA response element can confer inducibility by both alpha- and gamma-
A:Reference number: A31454; MUID:89128873; PMID:2492664
A:Accession: A31454
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-125 <REI>
A:CROSS-references: UNIPROT:P13164; GB:J04164; NID:g177801; PIDN:AAA35494.1; PID:g177802
Query Match 55.5%; Score 387; DB 2; Length 125;
Best Local Similarity 72.8%; Pred. No. 1.2e-33;
Matches 75; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
QY 24 KEEYEVAEMGAPHGASASVRTTVINMPREVSPDPHVWVSLFNTLPMNFCCLGFTAYAYSVK 83
Db 3 KEEBEVAVLGAPSTIDPRSTVINHSSETSPDPHVWVSLFNTLPMNFCCLGFTAFAYSVK 62
QY 84 SRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVITIVSVI 126
Db 63 SRDRKMGVDVTGAQAYASTAKCLNIWALILGILMTIGFILSLV 105
```

RESULT 5  
S00742

cytochrome-c oxidase (BC 1.9.3.1) chain I - Tetrahymena pyriformis mitochondrion  
C:Species: mitochondrion Tetrahymena pyriformis  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: S00742  
R:Ziaie, Z.; Suyama, Y.  
Curr. Genet. 12, 357-368, 1987

A:Title: The cytochrome oxidase subunit I gene of Tetrahymena: a 57 amino acid NH2-termini  
A:Reference number: S00742; MUID:88184706; PMID:2833363  
A:Accession: S00742  
A:Molecule type: DNA

A:Residues: 1-698 <ZIA>  
A:CROSS-references: UNIPROT:P11947; EMBL:X06133  
C:Genetics:  
A:Genome: mitochondrion  
A:Genetic code: SGC6

A:Start codon: ATA  
A:Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology  
C:Keywords: chromoprotein; copper; electron transfer; heme; iron; magnesium; membrane-associated transmembrane protein  
F:59-617/Domain: cytochrome-c oxidase chain I homology <COI>  
F:111-538/Binding site: heme a iron (His) (axial ligands) #status predicted  
F:401-450-451/Binding site: copper (His) #status predicted  
F:401-405/Cross-link: 1-histidyl-3-tyrosine (His-Tyr) #status predicted  
F:405/Binding site: oxygen (Tyr) #status predicted  
F:528/Binding site: magnesium (His) (shared with chain II) #status predicted  
F:536/Binding site: heme a3 iron (His) (axial ligand) #status predicted

Query Match 12.0%; Score 83.5; DB 1; Length 698;

Best Local Similarity 22.9%; Pred. No. 1;

Matches 27; Conservative 14; Mismatches 54; Indels 23; Gaps 3;

QY 3 HTSQAFITAAAGGQP-----PN-YERIKEEYEVAEMGAPHGASASVRTTVINMP 49

Db 375 HWQTFEFYAYGGDPILSQHLFWFFGHPEVYVLIPTFGFINNVPH-----NNT 424

QY 50 REVSVDPDHVWVSLFNTLPMNFCCLGFTAYAYSVKGRDRKMGVDVTGAQAYASTAKCLN 107

Db 425 RRVASKHHMIWAIYVMAYMGLVWGHMYLVGLDHRSTRMTYSTITTIMSPATIKVYN 482

RESULT 6  
AF1421

hypothetical membrane protein lmo2775 [imported] - Listeria monocytogenes (strain EGD-e)  
C:Species: Listeria monocytogenes  
C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004

C:Accession: AF1421  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Feihl, H.;

D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001

A:Authors: Kieft, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat

Ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AF1421  
A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-722 <GLA>

A:CROSS-references: UNIPROT:Q8Y3Q8; GB:NC\_003210; PIDN:CAD00988.1; PID:g16412275; GSPDB:C

A:Experimental source: strain EGD-e

C:Genetics:  
A:Gene: lmo2775

Query Match 11.9%; Score 83; DB 2; Length 722;

Best Local Similarity 21.8%; Pred. No. 1.2;

Matches 24; Conservative 25; Mismatches 47; Indels 14; Gaps 3;

QY 20 YERIKEEYEVAEMGAPHGASASVRTTVINMPREVSPDPHVWVSLFNTLPMNFCCLGFIAYA 79

Db 20 YERIKEEYEVAEMGAPHGASASVRTTVINMPREVSPDPHVWVSLFNTLPMNFCCLGFIAYA 79

Db 157 YQAPLKEPE-----QYGEVTTKSDVSWKYNIP-----LMTLLCFAILFVFTYY 204

Qy 80 YSVKSRDRKMWGDVTGAQAYASTAKCLN--ISTLVLSILMVVITIVSVII 127

Db 205 YLRYSKQRLVNRINGNSSELVTLMSLENKTIIFTLSVLAILITFVSIVL 254

RESULT 7

OPDP1

Cytochrome-c oxidase (EC 1.9.3.1) chain I - Paramacium sp. mitochondrion

N:Alternate names: cytochrome a3 polypeptide I; cytochrome a3 polypeptide I

C:Species: mitochondrion Paramacium sp.

C:Date: 31-Mar-1989 #sequence\_revision 31-Mar-1989 #text\_change 09-Jul-2004

C:Accession: A24988

R:Pritchard, A.E.; Seilhamer, J.J.; Cummings, D.J.

Gene 44, 243-253, 1986

A:Title: Paramacium mitochondrial DNA sequences and RNA transcripts for cytochrome oxidase

A:Reference number: A91555; MUID:87055241; PMID:3023187

A:Accession: A24988

A:Molecule type: DNA

A:Residues: 1-645 <PRI>

A:Cross-references: UNIPROT:P05489; GB:M15281; NID:G342944; PIDN:AAA79251.1; PID:g101962

A:Note: in GenBank entry ODPp1, release 109.0, PID:g1019626 assumes special genetic code

C:Genetics:

A:Gene: COI

A:Genome: mitochondrion

A:Genetic code: SGC6

A:Start codon: ATA

C:Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology

C:Keywords: chromoprotein; copper; electron transfer; heme; iron; magnesium; membrane-as

transmembrane protein

F:2-559/Domain: cytochrome-c oxidase chain I homology <COI>

F:54,480/Binding site: heme a iron (His) (axial ligands) #status predicted

F:343,392,393/Binding site: copper (His) #status predicted

F:343-347/Cross-link: 1'-histidyl-3'-tyrosine (His-Tyr) #status predicted

F:347/Binding site: oxygen (Tyr) #status predicted

F:470/Binding site: magnesium (His) (shared with chain II) #status predicted

F:478/Binding site: heme a3 iron (His) (axial ligand) #status predicted

Query Match 11.5%; Score 80; DB 1; Length 645;

Best Local Similarity 24.0%; Pred. No. 2.2;

Matches 30; Conservative 24; Mismatches 65; Indels 6; Gaps 4;

Qy 3 HTSQAFITPAAGGQPPNVERIKEEY---EVAEMGAP-HGSASVRTVINMPREVSVDPHV 58

Db 317 HWQTSFDFAYGGDPILFQHLFWFGHPDEVILIIPSGVANIVLPFVTM-RRMSSKHHM 375

Qy 59 VWSLFTLFWNFCCLGFTAYAYSVKSRDRKMWGDVTGAQAYASTAKCLNISTLVLSILMV 118

Db 376 IWAVYVMAYMGFVVGHHMVLVGLDHRSRNIYSTITIMICLPATIKLVN-WTLTLANAAI 434

Qy 119 VITIV 123

Db 435 HVDLV 439

RESULT 8

cytochrome-c oxidase (EC 1.9.3.1) chain I - Paramacium tetraurelia mitochondrion

C:Species: mitochondrion Paramacium tetraurelia

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C:Accession: S07751

R:Pritchard, A.E.; Seilhamer, J.J.; Mahalingam, R.; Sable, C.L.; Venuti, S.E.; Cummings, Nucleic Acids Res 18, 173-180, 1990

A:Title: Nucleotide sequence of the mitochondrial genome of Paramacium.

A:Reference number: S07725; MUID:90174913; PMID:2308823

A:Accession: S07751

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-645 <PRI>

A:Cross-references: UNIPROT:P05489; EMBL:X15917; NID:g13256; PIDN:CAA34030.1; PID:g57876

C:Genetics:

A:Gene: COI

A:Genome: mitochondrion

A:Genetic code: SGC6

A:Start codon: ATA

C:Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology

C:Keywords: chromoprotein; copper; electron transfer; heme; iron; magnesium; membrane-as

transmembrane protein

F:2-559/Domain: cytochrome-c oxidase chain I homology <COI>

F:54,480/Binding site: heme a iron (His) (axial ligands) #status predicted

F:343,392,393/Binding site: copper (His) #status predicted

F:343-347/Cross-link: 1'-histidyl-3'-tyrosine (His-Tyr) #status predicted

F:347/Binding site: oxygen (Tyr) #status predicted

F:470/Binding site: magnesium (His) (shared with chain II) #status predicted

F:478/Binding site: heme a3 iron (His) (axial ligand) #status predicted

Query Match 11.5%; Score 80; DB 1; Length 645;

Best Local Similarity 24.0%; Pred. No. 2.2;

Matches 30; Conservative 24; Mismatches 65; Indels 6; Gaps 4;

Qy 3 HTSQAFITPAAGGQPPNVERIKEEY---EVAEMGAP-HGSASVRTVINMPREVSVDPHV 58

Db 317 HWQTSFDFAYGGDPILFQHLFWFGHPDEVILIIPSGVANIVLPFVTM-RRMSSKHHM 375

Qy 59 VWSLFTLFWNFCCLGFTAYAYSVKSRDRKMWGDVTGAQAYASTAKCLNISTLVLSILMV 118

Db 376 IWAVYVMAYMGFVVGHHMVLVGLDHRSRNIYSTITIMICLPATIKLVN-WTLTLANAAI 434

Qy 119 VITIV 123

Db 435 HVDLV 439

RESULT 9

T09067

extensin-like protein NG5 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C:Accession: T09067

R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sc submitted to the EMBL Data Library, October 1997

A:Description: Sequence of the mouse major histocompatibility locus class III region.

A:Reference number: 216543

A:Accession: T09067

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-306 <ROW>

A:Cross-references: UNIPROT:O35449; EMBL:AF030001; NID:g2564945; PID:g2564955

C:Genetics:

A:Gene: NG5

A:Map position: 17

A:Introns: 7/1; 186/3; 248/3

Query Match 11.0%; Score 76.5; DB 2; Length 306;

Best Local Similarity 21.5%; Pred. No. 2.3;

Matches 29; Conservative 25; Mismatches 64; Indels 17; Gaps 4;

Qy 15 GQPPNVERIKEEYEVAEMGAPH-----GSASVRTVINMPR-----EVSVPDQHVWVSL 62

Db 167 GYPLQLQCTAYVPVYVGTPTAGTGGPQVSTLPPPGQGLALLEPRPPHDYMPI 226

Qy 63 FNTLFMNFCCL---GFTAYAYSVKSRDRKMWGDVTGAQAYASTAKCLNISTLVLSILMV 119

Db 227 --AVLTTCFCFPWPTGIIAIPKAVQRTALARGDLVSAEIASREARNFSISLAVGIAAMV 284

Qy 120 ITIVSVIIIVLNAQN 134

Db 285 LCTILTIVIIIAAQH 299

RESULT 10

T31092

probable voltage-gated sodium channel - Aiptasia pallida

C:Species: Aiptasia pallida

C:Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 09-Jul-2004

C;Accession: T31092  
R;White, G.B.; Pfahl, A.; Haddock, S.; Lamers, S.; Greenberg, R.M.; Anderson, P.A.V.  
Submitted to the EMBL Data Library, January 1998  
A;Description: Structure of a putative sodium channel from the sea anemone *Aiptasia pallida*  
A;Reference number: Z20975  
A;Accession: T31092  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1810 <WHI>  
A;Cross-references: UNIPROT:O44930; EMBL:AF041851; NID:g2791840; PID:g2791841; PIDN:AA89  
C;Genetics:  
A;Gene: NaI  
C;Superfamily: sodium channel protein

Query Match 10.8%; Score 75; DB 2; Length 1810;  
Best Local Similarity 24.4%; Pred. No. 22;  
Matches 33; Conservative 23; Mismatches 39; Indels 40; Gaps 8;

QY 19 NYERIKEEYEVAEMGA-----PHGSA---SVRTTIVNMPREV-SVPDH--VVW----- 60  
Db 1309 NFRLKKQYB--DFGALDVLLTSQRANFGTIRRAATKPKKVISRPENSMFLWFDVIH 1366  
QY 61 -SLFNTLFMNFCLGFIAYAYSVKSRDRKMVGDTVGAQAYA---STAKCLINISTLVLSIL 116  
Db 1367 SSRFETLMFFICLNIL-----VMIQHYGQKPAVEQALMIINLVFTGL 1410  
QY 117 MVVITIVSVIIIVLN 131  
Db 1411 FTLEAIRIVVLRHL 1425

RESULT 11  
A70839  
N;probable membrane protein - Mycobacterium tuberculosis (strain H37RV)  
C;Alternate names: membrane protein MLCL622 homolog  
C;Species: Mycobacterium tuberculosis  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C;Accession: A70839  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A;Authors: Squares, R.; Sultston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A;Reference number: A70500; MUID:98295987; PMID:9634230  
A;Accession: A70839  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-412 <COL>  
A;Cross-references: UNIPROT:O53655; GB:AL021928; GB:AL123456; NID:g3261522; PIDN:CAA1732  
A;Experimental source: strain H37RV  
C;Genetics:  
A;Gene: Rv0204c

Query Match 10.5%; Score 73.5; DB 2; Length 412;  
Best Local Similarity 33.8%; Pred. No. 6.5;  
Matches 23; Conservative 11; Mismatches 27; Indels 7; Gaps 3;

QY 60 WSLFNTLFMNFCLGFIAYAYSVKSRDRKMVGDTVGAQAYASTAKCLINISTLVLSIIMVV 119  
Db 258 WSLFNNI-ADVACLGFAAYA---AGDHASVGGI--AVAYAAARAVGTIPLMFGVLVVE 310  
QY 120 ITIVSVII 127  
Db 311 AVLVPGLV 318

RESULT 12  
S75757  
hypothetical protein sll1046 - *Synechocystis* sp. (strain PCC 6803)  
C;Species: *Synechocystis* sp.  
A;Variety: PCC 6803  
C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C;Accession: S75757  
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996  
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* s.  
A;Reference number: S74322; MUID:97061201; PMID:8905231  
A;Accession: S75757  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-84 <KAN>  
A;Cross-references: UNIPROT:P74772; EMBL:D64003; GB:AB001339; NID:g1001200; PIDN:BAAL049;  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 10.4%; Score 72.5; DB 2; Length 84;  
Best Local Similarity 29.3%; Pred. No. 1.5;  
Matches 24; Conservative 13; Mismatches 40; Indels 5; Gaps 2;

QY 54 VPDHVVMSLFNTLFMNFCC--LGFIAYAYSVKSRDRKMVGDTVGAQAYASTAKCLINISTL 111  
Db 6 VNYLAQSIIVTL---FCCPLGIVAIIRKASEVNSRLASGDYEGAVKASKEAKKFCWWSF 62  
QY 112 VLSILMVVITIVSVIIIVLNAQ 133  
Db 63 GAGIIFIAYFVLVIAAVFGQ 84

RESULT 13  
S40702  
hypothetical protein C07A9.10 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S40702  
R;Smith, M.  
submitted to the EMBL Data Library, December 1993  
A;Reference number: S40701  
A;Accession: S40702  
A;Molecule type: DNA  
A;Residues: 1-254 <SMI>  
A;Cross-references: UNIPROT:P34321; EMBL:Z29094; NID:g436440; PID:g436442  
C;Genetics:  
A;Introns: 61/3; 82/1; 184/3

Query Match 10.3%; Score 72; DB 2; Length 254;  
Best Local Similarity 19.1%; Pred. No. 5.5;  
Matches 35; Conservative 26; Mismatches 56; Indels 66; Gaps 7;

QY 1 MNHTSOAFITAASG---GPPN--YERIKEEYEVAEMG---APHGS-----ASVR 42  
Db 1 MHTDDRMVSHKKRPVGPMPRWTDLSRKEITTRDMGNIIITPWSQAKDRKAWKAVIR 60  
QY 43 TTVINMPREVSVDPHV-----VMSLFNTLFMNF- 70  
Db 61 TTETREPKNIIYKQVTVLFQANATISGPPVLPKPVKIHASSYLSLRNLGDDCFMNV 120  
QY 71 -----CCLGFI-AYAYSVKSRDRKMVGDTVGAQAYASTAKCLINISTLVLS 114  
Db 121 LQLLKSSPEDHFRTCCTGTHIELKILSGEKVDVGLRRMHYSKLHGRNCTALK 180  
QY 115 ILM 117  
Db 181 VLM 183

RESULT 14  
H97249  
protein containing aminopeptidase domain (iap family) [imported] - *Clostridium acetobutylicum*  
C;Species: *Clostridium acetobutylicum*  
C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C;Accession: H97249  
R;Nolling, J.; Berton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001

Search completed: June 18, 2005, 16:35:29  
Job time : 40 secs

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OM protein - protein search, using sw model

Run on: June 18, 2005, 16:28:00 ; Search time 43 Seconds  
(without alignments)  
237.835 Million cell updates/sec

Title: US-10-621-911A-2  
Perfect score: 697  
Sequence: 1 MNHTSQAFITAAAGGQPPNY.....VWITVSVIIIVLNAQLHT 137

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgm2\_6/ptodata/1/iaa/5A\_COMB.pap:\*\*
- 2: /cgm2\_6/ptodata/1/iaa/5B\_COMB.pap:\*\*
- 3: /cgm2\_6/ptodata/1/iaa/6A\_COMB.pap:\*\*
- 4: /cgm2\_6/ptodata/1/iaa/6B\_COMB.pap:\*\*
- 5: /cgm2\_6/ptodata/1/iaa/PCTUS\_COMB.pap:\*\*
- 6: /cgm2\_6/ptodata/1/iaa/backfiles.pap:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description          |
|------------|-------|-------------|--------|----|----------------------|
| 1          | 473   | 67.9        | 133    | 4  | US-09-370-838-124    |
| 2          | 473   | 67.9        | 133    | 4  | US-09-854-133-124    |
| 3          | 464   | 66.6        | 133    | 4  | US-09-461-912A-37    |
| 4          | 381   | 54.7        | 125    | 5  | PCT-US93-06829-2     |
| 5          | 376   | 53.9        | 125    | 5  | PCT-US93-06829-17    |
| 6          | 370   | 53.1        | 125    | 5  | PCT-US93-06829-13    |
| 7          | 370   | 53.1        | 125    | 5  | PCT-US93-06829-15    |
| 8          | 366   | 52.5        | 125    | 5  | PCT-US93-06829-16    |
| 9          | 365   | 52.4        | 125    | 5  | PCT-US93-06829-14    |
| 10         | 364   | 52.2        | 125    | 5  | PCT-US93-06829-12    |
| 11         | 72    | 10.3        | 690    | 3  | US-08-935-433-2      |
| 12         | 72    | 10.3        | 690    | 3  | US-09-553-132-2      |
| 13         | 72    | 10.3        | 706    | 4  | US-09-949-016-11394  |
| 14         | 71.5  | 10.3        | 318    | 2  | US-09-027-013-4      |
| 15         | 71.5  | 10.3        | 318    | 3  | US-09-244-233-4      |
| 16         | 69.5  | 10.0        | 746    | 4  | US-09-589-892B-2     |
| 17         | 68    | 9.8         | 219    | 2  | US-08-855-140-4      |
| 18         | 68    | 9.8         | 448    | 4  | US-09-323-195A-18    |
| 19         | 67.5  | 9.7         | 256    | 4  | US-09-270-767-46799  |
| 20         | 66.5  | 9.5         | 404    | 4  | US-09-252-991A-23011 |
| 21         | 66    | 9.5         | 240    | 3  | US-09-134-001C-4180  |
| 22         | 66    | 9.5         | 270    | 1  | US-08-347-471-4      |
| 23         | 66    | 9.5         | 310    | 4  | US-09-509-738C-24    |
| 24         | 65.5  | 9.4         | 444    | 4  | US-09-540-236-1993   |
| 25         | 65.5  | 9.4         | 539    | 4  | US-09-538-082-741    |
| 26         | 65    | 9.3         | 299    | 4  | US-09-520-781-28     |
| 27         | 65    | 9.3         | 391    | 4  | US-09-721-870-34     |

ALIGNMENTS

RESULT 1

US-09-370-838-124  
; Sequence 124, Application US/09370838  
; Patent No. 6444425

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Lodes, Michael J.

APPLICANT: Mohamath, Raodoh

APPLICANT: Secrist, Heather

TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF

TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.475C1

CURRENT APPLICATION NUMBER: US/09/370,838

CURRENT FILING DATE: 1999-08-09

EARLIER APPLICATION NUMBER: US 09/285,323

EARLIER FILING DATE: 1999-04-02

NUMBER OF SEQ ID NOS: 289

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 124

LENGTH: 133

TYPE: PRT

ORGANISM: Homo sapien

US-09-370-838-124

Query Match 67.9%; Score 473; DB 4; Length 133;

Best Local Similarity 70.3%; Pred. No. 6.9e-52;

Matches 90; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

Qy 1 MNHTSQAFITAAAGGQPPNYERKEEYEAEMGAPHGSASVRTTVINNPREVSPDHVW 60

Db 1 MNHTVQTFPPVNSGQPPNYEMLEKEHEVAVLGAPHNPAPTSTVIHIRSTSPDHVW 60

Qy 61 SLFNTLFMPCCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTVLGLMVVI 120

Db 61 SLFNTLFMPCCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTVLGLMVVI 120

Qy 121 TVIVPVLI 128

Db 121 TVIVPVLI 128

RESULT 2

US-09-854-133-124

; Sequence 124, Application US/09854133

; Patent No. 6759508

GENERAL INFORMATION:

APPLICANT: Lodes, Michael J.

APPLICANT: Mohamath, Raodoh

APPLICANT: Henderson, Robert A.

APPLICANT: Benson, Darin R.





CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/06829  
FILING DATE: 19930720  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/917,213  
FILING DATE: 07-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 15280-67  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 125 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-06829-17

Query Match 53.9%; Score 376; DB 5; Length 125;  
Best Local Similarity 62.4%; Pred. No. 1.2e-39;  
Matches 73; Conservative 17; Mismatches 17; Indels 10; Gaps 1;  
QY 24 KEEVEVAEMGAPHSASVRTTIVNMPREVSPDHVWSLNTLFMNFCCLGFIAYAVSVK 83  
Db 3 KEEHEVAVLGAPPSTILPRSTVINIHSETSVPDHGWSLNTLFNWCCLGFIAPAVSVK 62  
QY 84 SRDRKMGVDVTGAQAYASTAKCLNISTVLISILMV-----ITIVSVIIIVL 130  
Db 63 SRDRKMGVDVTGAQAYASTAKCLNIWALIGILMTIGFGASLVFGSVTVYHMLQII 119

RESULT 6  
PCT-US93-06829-13  
Sequence 13, Application PC/TUS9306829  
GENERAL INFORMATION:  
APPLICANT: Pavlakis, George N.  
APPLICANT: Constantoulakis, Pantelis  
APPLICANT: Felber, Barbara K.  
TITLE OF INVENTION: INHIBITION OF RETROVIRAL EXPRESSION BY  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend  
STREET: One Market Plaza, Steuart St. Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/06829  
FILING DATE: 19930720  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/917,213

FILING DATE: 07-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 15280-67  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 125 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-06829-13

Query Match 53.1%; Score 370; DB 5; Length 125;  
Best Local Similarity 69.9%; Pred. No. 7e-39;  
Matches 72; Conservative 13; Mismatches 18; Indels 0; Gaps 0;  
QY 24 KEEVEVAEMGAPHSASVRTTIVNMPREVSPDHVWSLNTLFMNFCCLGFIAYAVSVK 83  
Db 3 KEEHEVAVLGAPPSTILPRSTVINIHSETSVPDHGWSLNTLFNWCCLGFIAPAVSVK 62  
QY 84 SRDRKMGVDVTGAQAYASTAKCLNISTVLISILMVITIVSVI 126  
Db 63 SRDRKMGVDVTGAQAYASTAKCLNIWALIGILMTIGFILSLV 105

RESULT 7  
PCT-US93-06829-15  
Sequence 15, Application PC/TUS9306829  
GENERAL INFORMATION:  
APPLICANT: Pavlakis, George N.  
APPLICANT: Constantoulakis, Pantelis  
APPLICANT: Felber, Barbara K.  
TITLE OF INVENTION: INHIBITION OF RETROVIRAL EXPRESSION BY  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend  
STREET: One Market Plaza, Steuart St. Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/06829  
FILING DATE: 19930720  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/917,213  
FILING DATE: 07-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 15280-67  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 125 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

## PCT-US93-06829-15

Query Match 53.1%; Score 370; DB 5; Length 125;  
Best Local Similarity 69.9%; Pred. No. 7e-39;  
Matches 72; Conservative 13; Mismatches 18; Indels 0; Gaps 0;  
Qy 24 KEEYEVAEMGAPHGSASVTRTINMPREVSVPDHVWMSLFTLPMNFCCIGFTAYAYSVK 83  
Db 3 KEEHEVAVLGAPPSTILPRSGAINHSETSPDHVWMSLFTLFLNWCCIGFTAFAYSVK 62  
Qy 84 SRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVITIVSVI 126  
Db 63 SRDRKMGVDVTGAQAYASTAKCLNIWALILGILMTIGFILSLV 105

## RESULT 8

PCT-US93-06829-16  
; Sequence 16, Application PC/TUS9306829  
; GENERAL INFORMATION:  
; APPLICANT: Pavlakis, George N.  
; APPLICANT: Constantoulakis, Pantelis  
; APPLICANT: Felber, Barbara K.  
; TITLE OF INVENTION: INHIBITION OF RETROVIRAL EXPRESSION BY  
; TITLE OF INVENTION: INTERFERON-INDUCED CELLULAR GENES AND PROTEINS  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend  
; STREET: One Market Plaza, Steuart St. Tower  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/06829  
; FILING DATE: 19930720  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/917,213  
; FILING DATE: 07-JUL-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parmelee, Steven W.  
; REGISTRATION NUMBER: 31,990  
; REFERENCE/DOCKET NUMBER: 15280-67  
; TELEPHONE: 206-467-9600  
; TELEFAX: 415-543-5043  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 125 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
PCT-US93-06829-16

Query Match 52.5%; Score 366; DB 5; Length 125;  
Best Local Similarity 69.9%; Pred. No. 2.3e-38;  
Matches 72; Conservative 13; Mismatches 18; Indels 0; Gaps 0;  
Qy 24 KEEYEVAEMGAPHGSASVTRTINMPREVSVPDHVWMSLFTLPMNFCCIGFTAYAYSVK 83  
Db 3 KEEHEVAVLGAPPSTILPRSTVINHSETSPDHVWMSLFTLFLNWCCIGFTAFAYSVK 62  
Qy 84 SRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVITIVSVI 126  
Db 63 SGARKMGVDVTGAQAYASTAKCLNIWALILGILMTIGFILSLV 105

## RESULT 9

PCT-US93-06829-14  
; Sequence 14, Application PC/TUS9306829  
; GENERAL INFORMATION:  
; APPLICANT: Pavlakis, George N.  
; APPLICANT: Constantoulakis, Pantelis  
; APPLICANT: Felber, Barbara K.  
; TITLE OF INVENTION: INHIBITION OF RETROVIRAL EXPRESSION BY  
; TITLE OF INVENTION: INTERFERON-INDUCED CELLULAR GENES AND PROTEINS  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend  
; STREET: One Market Plaza, Steuart St. Tower  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/06829  
; FILING DATE: 19930720  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/917,213  
; FILING DATE: 07-JUL-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parmelee, Steven W.  
; REGISTRATION NUMBER: 31,990  
; REFERENCE/DOCKET NUMBER: 15280-67  
; TELEPHONE: 206-467-9600  
; TELEFAX: 415-543-5043  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 125 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
PCT-US93-06829-14  
Query Match 52.4%; Score 365; DB 5; Length 125;  
Best Local Similarity 69.9%; Pred. No. 3e-38;  
Matches 72; Conservative 13; Mismatches 18; Indels 0; Gaps 0;  
Qy 24 KEEYEVAEMGAPHGSASVTRTINMPREVSVPDHVWMSLFTLPMNFCCIGFTAYAYSVK 83  
Db 3 KEEHEVAVLGAPPSTILPRSTVINHSETSPDHVWMSLFTLFLNWCCIGFTAFAYSVK 62  
Qy 84 SRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVITIVSVI 126  
Db 63 SRDRKMGVDVTGAQAYASTAKCLNIWALILGILMTIGFILSLV 105

## RESULT 10

PCT-US93-06829-12  
; Sequence 12, Application PC/TUS9306829  
; GENERAL INFORMATION:  
; APPLICANT: Pavlakis, George N.  
; APPLICANT: Constantoulakis, Pantelis  
; APPLICANT: Felber, Barbara K.  
; TITLE OF INVENTION: INHIBITION OF RETROVIRAL EXPRESSION BY  
; TITLE OF INVENTION: INTERFERON-INDUCED CELLULAR GENES AND PROTEINS  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend  
; STREET: One Market Plaza, Steuart St. Tower  
; CITY: San Francisco  
; STATE: CA

```

; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06829
; FILING DATE: 19930720
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/917,213
; FILING DATE: 07-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 15280-67
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 208-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 125 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US93-06829-12

Query Match 52.2%; Score 364; DB 5; Length 125;
Best Local Similarity 69.9%; Pred. No. 4e-38;
Matches 72; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

Qy 24 KEEVEAEMGAPHGASVRTVINMPREVDPDHVVWSLNTLFNFCCLGFIAYAVSVK 83
Db 3 KEEVEAVIGAPPSTILPRSTVINHSYVPGAVVWSLNTLFNFCCLGFIAYAVSVK 62

Qy 84 SRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVVITVSVI 126
Db 63 SRDRKMGVDVTGAQAYASTAKCLNIWAILILGILMTIGFILSIV 105

RESULT 11
US-08-935-433-2
; Sequence 2, Application US/08935433
; Patent No. 6319688
; GENERAL INFORMATION:
; APPLICANT: FEILD, JOHN
; TITLE OF INVENTION: A HUMAN SODIUM DEPENDENT PHOSPHATE
; TITLE OF INVENTION: TRANSPORTER (IPT-1)
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/935,433
; FILING DATE: 23-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/044,974
; FILING DATE: 28-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F

; COUNTRY: USA
; ZIP: 94105-1492
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 690 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-935-433-2

Query Match 10.3%; Score 72; DB 3; Length 690;
Best Local Similarity 20.6%; Pred. No. 4.3;
Matches 33; Conservative 34; Mismatches 61; Indels 32; Gaps 6;

Qy 8 FITAASGGQPPNYRIKEEYEAEMGAPHGASV-----RTVINMPREVSV----- 55
Db 17 YLEGAAGQQPTAPDKSKETNKTNDTEAPVTKIELLPSYSTATLIDETEVDDPWNLTQ 76

Qy 56 -DHVVWSLNTLFNFC-----CLGFIAY---AYSVKSRDRKMGVDVTGAQAYAS 101
Db 77 DSGIKWSEDTGKILCFQIGIRLILLGLFYFVCSLDTLSSAFQLVGGKMACQFFSN 136

Qy 102 TAKCLN-ISTLVLSILMWVI-----TIVSVIIIVLNAQNL 135
Db 137 SSIMSNPLGLVIGVLTVLVQSSSTSTSIIVVSMVSSSL 176

RESULT 12
US-09-553-132-2
; Sequence 2, Application US/09553132
; Patent No. 6350858
; GENERAL INFORMATION:
; APPLICANT: FEILD, JOHN
; TITLE OF INVENTION: A HUMAN SODIUM DEPENDENT PHOSPHATE
; TITLE OF INVENTION: TRANSPORTER (IPT-1)
; FILE REFERENCE: -GH-70006-D1
; CURRENT APPLICATION NUMBER: US/09/553,132
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 60/044,974
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/935,433
; PRIOR FILING DATE: 1997-09-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 690
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-553-132-2

Query Match 10.3%; Score 72; DB 3; Length 690;
Best Local Similarity 20.6%; Pred. No. 4.3;
Matches 33; Conservative 34; Mismatches 61; Indels 32; Gaps 6;

Qy 8 FITAASGGQPPNYRIKEEYEAEMGAPHGASV-----RTVINMPREVSV----- 55
Db 17 YLEGAAGQQPTAPDKSKETNKTNDTEAPVTKIELLPSYSTATLIDETEVDDPWNLTQ 76

Qy 56 -DHVVWSLNTLFNFC-----CLGFIAY---AYSVKSRDRKMGVDVTGAQAYAS 101
Db 77 DSGIKWSEDTGKILCFQIGIRLILLGLFYFVCSLDTLSSAFQLVGGKMACQFFSN 136

Qy 102 TAKCLN-ISTLVLSILMWVI-----TIVSVIIIVLNAQNL 135
Db 137 SSIMSNPLGLVIGVLTVLVQSSSTSTSIIVVSMVSSSL 176

RESULT 13
```

```
US-09-949-016-11394
; Sequence 11394, Application US/09949016
; Patent No. 5812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFECTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11394
; LENGTH: 706
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11394

Query Match      10.3%; Score 72; DB 4; Length 706;
Best Local Similarity 20.6%; Pred. No. 4.4; Indels 61; Mismatches 34; Gaps 6;
Matches 33; Conservative

QY 8 FITAAGGQPPNYRIKEEYVAEMGAPHSASV-----RTVINMPREVSVP----- 55
DB 33 YLEGAAGQQTAPDKSKETKNTDTEAPVTKIELLPSTATLIDETVEDDPWNLPTLQ 92
QY 56 -DHVWSLFTLFWNFC-----CLGFIAY--AYSVKGRDRKMGVDVTGAQAYAS 101
DB 93 DSGIKMSERDTGKILCFQIGRLLILLGLFYFFVCSLDLSSAFOLVGGKMGAGOFFSN 152
QY 102 TAKCLN-ISTVLISLMVVI-----TIVSVIIVLNAQNL 135
DB 153 SSIMSNNLLGLVIGLVTVLVQSSSTSTSVMSVSSLL 192

RESULT 14
US-09-027-013-4
; Sequence 4, Application US/09027013
; Patent No. 5962302
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN N-ACETYLNEURAMINATE LYASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,013
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0462 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: GI 1016806
```

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; REFERENCE/DOCKET NUMBER: PF-0462 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: GI 1016806
US-09-027-013-4

Query Match      10.3%; Score 71.5; DB 2; Length 318;
Best Local Similarity 19.0%; Pred. No. 1.7;
Matches 19; Conservative 21; Mismatches 29; Indels 31; Gaps 3;

QY 21 ERIKEEYVAEMGAPHSASVRTTIVINMPREVSVPDHVWSLFTLFWNFCCLGPF---IA 77
DB 199 ERVKRAY-----PDHLIWAGFDEMMLPACSLGIDGAIG 231
QY 78 YAVSVKSRDRKMGVDVTGAQAYASTAKCLNIST-LVLSIL 116
DB 232 STFNVAKRARQIFELSKAGKYDEALEVQHVTVNDLIAGIL 271

RESULT 15
US-09-244-233-4
; Sequence 4, Application US/09244233
; Patent No. 6030824
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN N-ACETYLNEURAMINATE LYASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/244,233
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/027,013
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0462 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: GI 1016806
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US-09-244-233-4

Query Match 10.3%; Score 71.5; DB 3; Length 318;  
 Best Local Similarity 19.0%; Pred. No. 1.7;  
 Matches 19; Conservative 21; Mismatches 29; Indels 31; Gaps 3;  
 QY 21 ERIKEEYVAEMGAPHGASVTTTNNPREVSVDHVVWSLFTLFNFFCCLGF---IA 77  
 Db 199 ERVKRAY-----PDHLIWAGFDEMMLPACSLGIDGAIG 231  
 QY 78 VAYSVKSRDRKMVGDTVGAQAYASTAKCLNIST-LVLSIL 116  
 Db 232 STFNVNAXRQIFELSKAGKYDEALEVCHVTNDLIAGIL 271

Search completed: June 18, 2005, 16:36:17  
 Job time : 44 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2005, 16:12:19 ; Search time 161 Seconds  
(without alignments)  
329.107 Million cell updates/sec

Title: US-10-621-911A-2  
Perfect score: 697  
Sequence: 1 MNHTSQAFITRAGGQPPNY.....VVITIVSVIIIVLNAQNLT 137

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 697   | 100.0       | 137    | 5     | ABG30945 Mouse GCR |
| 2          | 697   | 100.0       | 137    | 8     | ADJ76155 Marker ge |
| 3          | 697   | 100.0       | 173    | 8     | ABO84418 Mouse can |
| 4          | 646   | 92.7        | 137    | 7     | AD663837 Rat Prote |
| 5          | 646   | 92.7        | 137    | 7     | ADD46415 Rat Prote |
| 6          | 497   | 71.3        | 144    | 8     | AD126260 Mouse Fra |
| 7          | 473   | 67.9        | 133    | 2     | AAY29544 Human lun |
| 8          | 473   | 67.9        | 133    | 3     | AB444556 Human lun |
| 9          | 473   | 67.9        | 133    | 4     | AAE13797 Human lun |
| 10         | 473   | 67.9        | 133    | 6     | ABR41053 Human MAP |
| 11         | 473   | 67.9        | 133    | 7     | ADD66432 Human lun |
| 12         | 473   | 67.9        | 133    | 7     | AD663839 Human Pro |
| 13         | 473   | 67.9        | 133    | 7     | ADD46417 Human Pro |
| 14         | 473   | 67.9        | 133    | 7     | AD663839 Human Pro |
| 15         | 473   | 67.9        | 143    | 5     | ABP43105 Human ova |
| 16         | 465   | 66.7        | 133    | 6     | ABR41051 Human MAP |
| 17         | 464   | 66.6        | 133    | 3     | AA933594 Protein e |
| 18         | 464   | 66.6        | 133    | 6     | ABR41052 Human MAP |
| 19         | 461   | 65.1        | 143    | 4     | ABG11590 Novel hum |
| 20         | 454   | 65.1        | 132    | 6     | ABR41089 Human MAP |
| 21         | 454   | 65.1        | 132    | 6     | ABO25123 Human 1-8 |
| 22         | 454   | 65.1        | 168    | 4     | AB23517 Novel hum  |
| 23         | 453   | 65.0        | 132    | 6     | ABR41088 Human MAP |
| 24         | 453   | 65.0        | 132    | 8     | AD107644 Human 1-8 |
| 25         | 453   | 65.0        | 156    | 7     | ADE09084 Novel pro |

|    |       |      |     |   |          |                    |
|----|-------|------|-----|---|----------|--------------------|
| 26 | 452   | 64.8 | 146 | 7 | ADE81103 | Ad81103 Bovine 1-  |
| 27 | 452   | 64.8 | 146 | 8 | ADI34857 | Adi34857 Bovine pr |
| 28 | 450   | 64.6 | 132 | 5 | ABP64706 | Abp64706 Human pr  |
| 29 | 450   | 64.6 | 132 | 8 | AD126256 | Ad126256 Human Fra |
| 30 | 450   | 64.6 | 132 | 8 | AD107646 | Ad107646 Human 1-8 |
| 31 | 450   | 64.6 | 132 | 8 | ABO84419 | ABO84419 Human can |
| 32 | 449   | 64.4 | 132 | 6 | ABR92090 | ABr92090 Human cer |
| 33 | 449   | 64.4 | 132 | 6 | ABR41050 | ABr41050 Human MAP |
| 34 | 449   | 64.4 | 132 | 8 | ADQ29673 | Adq29673 Human col |
| 35 | 449   | 64.4 | 132 | 8 | ABM81208 | ABm81208 Tumour-as |
| 36 | 449   | 64.4 | 132 | 8 | ADP23176 | Adp23176 PRO polyp |
| 37 | 448   | 64.3 | 145 | 4 | AAW40509 | AAw40509 Human pol |
| 38 | 447   | 64.1 | 132 | 4 | AAW38723 | AAw38723 Human pol |
| 39 | 442   | 63.4 | 124 | 4 | ABG11589 | ABg11589 Novel hum |
| 40 | 429.5 | 61.6 | 132 | 7 | ADE95522 | Ad95522 Human NOV  |
| 41 | 429.5 | 61.6 | 132 | 7 | ADE95524 | Ad95524 Human NOV  |
| 42 | 426.5 | 61.2 | 131 | 5 | ABP42194 | ABp42194 Human ova |
| 43 | 412.5 | 59.2 | 155 | 8 | ADP83527 | Adp83527 Breast sp |
| 44 | 388.5 | 55.7 | 107 | 8 | AD126262 | Ad126262 Mouse Fra |
| 45 | 387   | 55.5 | 125 | 4 | ABB50284 | Abb50284 IFN-induc |

ALIGNMENTS

RESULT 1  
ABG30945  
ID ABG30945 standard; protein; 137 AA.  
AC ABG30945;  
XX  
DT 21-OCT-2002 (first entry)  
XX  
DE Mouse GCR1/Fragilis protein.  
XX  
KW Mouse; GCR1; Fragilis; GCR2; Stella; pluripotent cell; PGC; transgenic;  
KW primordial germ cell; germ tissue development; embryonic stem cell;  
KW embryonic germ cell.  
XX  
OS Mus sp.  
XX  
FH Key  
FT Region  
FT Location/Qualifiers  
FT 12..28  
FT /note= "Anti-peptide antibody designed against this  
FT sequence"  
FT 85..100  
FT /note= "Anti-peptide antibody designed against this  
FT sequence"

WO200257307-A2.  
25-JUL-2002.  
18-JAN-2002; 2002WO-GB0000215.  
18-JAN-2001; 2001GB-00001300.  
(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.  
Saitou M, Surani A;  
WPI; 2002-590719/63.  
N-PSDB; ABK90152.  
GCR1 (Fragilis) and GCR2 (Stella) genes, useful for identifying and/or  
isolating a pluripotent cell e.g., primordial germ cell.  
Claim 13; Fig 1; 85pp; English.  
The present invention relates to a new GCR1 (Fragilis) or GCR2 (Stella)  
polypeptide, or its fragment, homologue, variant or derivative. The  
homologue of, or antibody specific for, GCR1 or GCR2 is useful for  
identifying and/or isolating a pluripotent cell, particularly PGC

CC (primordial germ cell) for studying germ tissue development and  
CC generation of transgenic animals, as well as embryonic stem cells or  
CC embryonic germ cells. The present amino acid sequence represents the  
CC mouse GCRI/Fragilis protein of the invention  
XX  
SQ Sequence 137 AA;  
  
Query Match 100.0%; Score 697; DB 5; Length 137;  
Best Local Similarity 100.0%; Pred. No. 5.1e-79;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MNHTSQAFITAAAGGQPPNYERIKEEYEVAEMGAPHGASVTRTVINMPREVSVPDHWVW 60  
DB 1 MNHTSQAFITAAAGGQPPNYERIKEEYEVAEMGAPHGASVTRTVINMPREVSVPDHWVW 60  
  
QY 61 SLFNTLFMNFCCGFIAYAYSVKSRDRKMVGDTVGAQAYASTAKCLNISTLVLSILMVVI 120  
DB 61 SLFNTLFMNFCCGFIAYAYSVKSRDRKMVGDTVGAQAYASTAKCLNISTLVLSILMVVI 120  
  
QY 121 TIVSVIIIVLNAQNLT 137  
DB 121 TIVSVIIIVLNAQNLT 137  
  
RESULT 2  
ADJ76155  
ID ADJ76155 standard; protein; 137 AA.  
XX  
AC ADJ76155;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Marker gene related amino acid sequence SEQ ID NO:1407.  
XX  
KW bronchial asthma; chronic obstructive pulmonary disease;  
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;  
KW gene therapy; marker.  
XX  
OS Mus musculus.  
XX  
PN EP1394274-A2.  
XX  
PD 03-MAR-2004.  
XX  
TF 04-AUG-2003; 2003EP-00254857.  
XX  
PR 06-AUG-2002; 2002JP-00229312.  
PR 20-MAR-2003; 2003JP-00077212.  
XX  
PA (GENO-) GENOX RES INC.  
XX  
PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;  
XX  
DR WPI; 2004-193155/19.  
XX  
PT Testing for bronchial asthma or chronic obstructive pulmonary disease by  
PT comparing the expression level of a marker gene in a biological sample  
PT from a subject with the expression level of the gene in a sample from a  
PT healthy subject.  
XX  
PS Claim 16; SEQ ID NO 1407; 241pp; English.  
XX  
CC The present invention describes a method of testing for bronchial asthma  
CC or chronic obstructive pulmonary disease. The method comprises  
CC determining the expression level of a marker gene in a biological sample  
CC from a subject, comparing the expression level determined with the  
CC expression level of the marker gene in a biological sample from a healthy  
CC subject, and judging whether the subject has bronchial asthma or chronic  
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of  
CC genes (S1) whose expression levels increase when respiratory epithelial  
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)  
CC whose expression levels decrease when respiratory epithelial cells are  
CC stimulated with interleukin-13. Also described: (1) a reagent (I) for

CC testing for bronchial asthma or chronic obstructive pulmonary disease;  
CC (2) a kit for screening for a candidate compound for a therapeutic agent  
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)  
CC an animal model for bronchial asthma or chronic obstructive pulmonary  
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a  
CC method for producing an animal model for bronchial asthma or chronic  
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial  
CC asthma or chronic obstructive pulmonary disease, comprising the compound,  
CC a marker gene or an antisense nucleic acid corresponding to a portion of  
CC the marker gene, a ribozyme, a polynucleotide that suppresses the  
CC expression of the gene through an RNAi effect or an antibody recognising  
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for  
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a  
CC probe has been immobilised to assay a marker gene. (I) has respiratory  
CC and antiasthmatic activities, and can be used in gene therapy. The method  
CC is useful for testing for or screening for a therapeutic agent for  
CC bronchial asthma or chronic obstructive pulmonary disease. The present  
CC sequence is used in the exemplification of the present invention.  
XX  
SQ Sequence 137 AA;  
  
Query Match 100.0%; Score 697; DB 8; Length 137;  
Best Local Similarity 100.0%; Pred. No. 5.1e-79;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MNHTSQAFITAAAGGQPPNYERIKEEYEVAEMGAPHGASVTRTVINMPREVSVPDHWVW 60  
DB 1 MNHTSQAFITAAAGGQPPNYERIKEEYEVAEMGAPHGASVTRTVINMPREVSVPDHWVW 60  
  
QY 61 SLFNTLFMNFCCGFIAYAYSVKSRDRKMVGDTVGAQAYASTAKCLNISTLVLSILMVVI 120  
DB 61 SLFNTLFMNFCCGFIAYAYSVKSRDRKMVGDTVGAQAYASTAKCLNISTLVLSILMVVI 120  
  
QY 121 TIVSVIIIVLNAQNLT 137  
DB 121 TIVSVIIIVLNAQNLT 137  
  
RESULT 3  
ABO84418  
ID ABO84418 standard; protein; 173 AA.  
XX  
AC ABO84418;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Mouse cancer-associated protein MP14-034.1.  
XX  
KW Mouse; cancer-associated protein; cytostatic; cancer; leukaemia;  
KW lymphoma; CAP.  
XX  
OS Mus musculus.  
XX  
PN WO2004074320-A2.  
XX  
PD 02-SEP-2004.  
XX  
PF 17-FEB-2004; 2004WO-US0004730.  
XX  
PR 14-FEB-2003; 2003US-00367094.  
PR 14-MAR-2003; 2003US-0038838.  
PR 15-APR-2003; 2003US-00417375.  
PR 13-JUN-2003; 2003US-00461862.  
PR 15-SEP-2003; 2003US-00663431.  
PR 15-DEC-2003; 2003US-00737318.  
XX  
PA (SAGR-) SAGRES DISCOVERY INC.  
XX  
PI Morris DW, Morris DW, Malandro MS;  
XX  
DR WPI; 2004-652914/63.  
DR N-PSDB; ABO32561.  
XX





XX AC ADD46415;  
XX DT 29-JAN-2004 (first entry)  
XX DE Rat Protein CAA43655, SEQ ID NO 12095.  
XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
XX OS chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX PN Rattus norvegicus.  
XX PD W02003016475-A2.  
XX PF 27-FEB-2003.  
XX PF 14-AUG-2002; 2002WO-US025765.  
XX PR 14-AUG-2001; 2001US-0312147P.  
XX PR 01-NOV-2001; 2001US-0346382P.  
XX PR 26-NOV-2001; 2001US-0333347P.  
XX PA (GEMO) GEN HOSPITAL CORP.  
XX PA (FARB) BAYER AG.  
XX PI Woolf C, D'urso D, Befort K, Costigan M;  
XX DR WPI; 2003-268312/26.  
XX DR GENBANK; CAA43655.  
XX DT New composition comprising two or more isolated polypeptides, useful for  
XX PT preparing a medicament for treating pain in an animal.  
XX PS Claim 1; Page; 1017pp; English.  
XX CC The invention discloses a composition comprising two or more isolated rat  
XX CC or human polynucleotides or a polynucleotide which represents a fragment,  
XX CC derivative or allelic variation of the nucleic acid sequence. Also  
XX CC claimed are a vector comprising the novel polynucleotide, a host cell  
XX CC comprising the vector, a method for identifying a nucleotide sequence  
XX CC which is differentially regulated in an animal subjected to pain and a  
XX CC kit to perform the method, an array, a method for identifying an agent  
XX CC that increases or decreases the expression of the polynucleotide sequence  
XX CC that is differentially expressed in neuronal tissue of a first animal  
XX CC subjected to pain, a method for identifying a compound which regulates  
XX CC the expression of a polynucleotide sequence which is differentially  
XX CC expressed in an animal subjected to pain, a method for identifying a  
XX CC compound that regulates the activity of one or more of the  
XX CC polynucleotides, a method for producing a pharmaceutical composition, a  
XX CC method for identifying a compound or small molecule that regulates the  
XX CC activity in an animal of one or more of the polypeptides given in the  
XX CC specification, a method for identifying a compound useful in treating  
XX CC pain and a pharmaceutical composition comprising the one or more  
XX CC polypeptides or their antibodies. The polynucleotide or the compound that  
XX CC modulates its activity is useful for preparing a medicament for treating  
XX CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
XX CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
XX CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
XX CC the specification) which is differentially expressed during pain. Note:  
XX CC The sequence data for this patent did not form part of the printed  
XX CC specification, but was obtained in electronic form directly from WIPO at  
XX CC ftp.wipo.int/pub/published\_ppt\_sequences.  
XX SQ Sequence 137 AA;  
Query Match 92.7%; Score 646; DB 7; Length 137;  
Best Local Similarity 89.8%; Pred. No. 1.3e-72;  
Matches 123; Conservative 9; Mismatches 5; Indels 0; Gaps 0;  
QY 1 MNHTSQAFITAAAGGQPPNYERKEEYEAEMGAPHGASVRRVTINMPREVSVPDHVW 60  
DB 1 MNHTSQAFVNAATGGQPPNYERKEEYEVSELGAPHGASVRRVTINMPREVSVPDHVW 60

QY 61 SLFNTLFMNFCCIGFIAYAYSVKSRDKWVGDTGAQAYASTAKCLNISTLVLSILMWVI 120  
DB 61 SLFNTLFMNFCCIGFIAYAYSVKSRDKWVGDTGAQAYASTAKCLNISTLVLSILMWVI 120  
QY 121 TIVSVIIIVLNAQNLT 137  
DB 121 TIVTVVIIALNAPRLQT 137  
RESULT 6  
ADI26260  
ID ADI26260 standard; protein; 144 AA.  
XX AC ADI26260;  
XX DT 22-APR-2004 (first entry)  
XX DE Mouse Fragilis 2 amino acid sequence SEQ ID NO:10.  
XX KW Fragilis; pluripotent cell; cytostatic; gene therapy; tumour;  
XX OS choriocarcinoma; carcinoma; leiomyosarcoma; mouse.  
XX PN Mus musculus.  
XX PN W02004007723-A2.  
XX PD 22-JAN-2004.  
XX PF 17-JUL-2003; 2003WO-GE003093.  
XX PR 17-JUL-2002; 2002GB-00016727.  
XX PR 19-JUL-2002; 2002US-0397310P.  
XX PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.  
XX PI Saitou M, Surani A;  
XX DR WPI; 2004-122953/12.  
XX DR N-PSDB; ADI26259.  
XX PT New polypeptide comprising a human Stella or Fragilis amino acid  
XX PT sequence, useful for treating or preventing testis, colon, stomach, germ  
XX PT cell, choriocarcinoma, lung, large cell carcinoma, uterus, and  
XX PT leiomyosarcoma.  
XX PS Claim 3; SEQ ID NO 10; 189pp; English.  
XX CC The present invention describes a polypeptide (1) comprising a human  
XX CC Stella (SEQ ID No. 4, ADI26254) or Fragilis (SEQ ID No. 6, ADI26256)  
XX CC amino acid sequence, its fragment, homologue, variant or derivative. Also  
XX CC described: (1) a nucleic acid encoding (1), or its complement; (2) a  
XX CC vector comprising the nucleic acid sequence; (3) a host cell comprising  
XX CC the nucleic acid sequence; (4) a method for producing (1); (5) a method  
XX CC for identifying a pluripotent cell; (6) an antibody capable of binding  
XX CC specifically to (1); (7) a pluripotent cell identified by the method; (8)  
XX CC a method of treatment or prophylaxis of a disease in an individual; (9) a  
XX CC method of diagnosis or a disease; (10) a method of identifying a molecule  
XX CC capable of binding to Stella or Fragilis; (11) a method of identifying a  
XX CC modulator, preferably an agonist or antagonist of Stella or Fragilis;  
XX CC (12) a modulator of Stella or Fragilis; (13) a transgenic non-human  
XX CC animal; (14) a cell or tissue from the transgenic non-human animal; and  
XX CC (15) a nucleic acid construct for functionally disrupting a Stella and/or  
XX CC Fragilis gene in a host cell. (1) has cytostatic activity, and can be  
XX CC used in gene therapy. The polypeptide (1), nucleic acid and methods are  
XX CC useful for treating or preventing testis tumour, colon tumour, stomach,  
XX CC germ cell tumours, choriocarcinoma, lung, large cell carcinoma, uterus,  
XX CC and leiomyosarcoma. The antibody is useful for the identification and/or  
XX CC isolation of a pluripotent cell. The transgenic non-human animal is  
XX CC useful for identifying a compound, which is capable of interacting  
XX CC specifically with a Stella or Fragilis protein. The present sequence  
XX CC represents a mouse Fragilis 2 amino acid sequence, which is used in the  
XX CC exemplification of the present invention.

SQ Sequence 144 AA;  
Query Match 71.3%; Score 497; DB 8; Length 144;  
Best Local Similarity 71.7%; Pred. No. 7.4e-54;  
Matches 99; Conservative 13; Mismatches 20; Indels 6; Gaps 2;  
QY 1 MNHTSQAFITAAAGCGPPNYERIKEEYEVAEMGAPHGASVTRTTVINMPREVSVPDHVW 60  
DB 1 MSHNSQAFI-STNAGLPSPSYETIKEEYGVTELGEPSNSAVVTRTTVINMPREVSVPDHVW 59  
QY 61 SLFNTLFMNFCCGLGFIAYAYSVKSRDRKMVGDTVGAQAYASTAKCLNISTLVLSILMVVI 120  
DB 60 SLFNTLFMNFCCGLGFIAYAYSVKSRDRKMVGDTVGAQAYASTAKCLNISTLVLSILMVII 119  
QY 121 TIV-----SVIIVLNAQ 133  
DB 120 CIIIFSTTSVVVFQSFQAQ 137  
RESULT 7  
ID AAY29544 standard; protein; 133 AA.  
AC AAY29544;  
XX  
DT 13-OCT-1999 (first entry)  
DE Human lung tumour protein SALT-T8 predicted amino acid sequence.  
XX  
KW Human; lung tumour protein; therapy; diagnosis; lung cancer; vaccine;  
KW immunotherapy; detection; inhibition.  
XX  
OS Homo sapiens.  
XX  
PN WO9938973-A2.  
PD 05-AUG-1999.  
XX  
PF 26-JAN-1999; 99WO-US001642.  
XX  
PR 28-JAN-1998; 98US-00015022.  
PR 28-JAN-1998; 98US-00015029.  
PR 18-MAR-1998; 98US-00040828.  
PR 18-MAR-1998; 98US-00040831.  
PR 23-JUL-1998; 98US-00122191.  
PR 23-JUL-1998; 98US-00122192.  
PR 22-DEC-1998; 98US-00219245.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Reed SG, Lodes MJ, Frudakis TN, Mohamath R;  
XX  
DR WPI; 1999-479187/40.  
DR N-PSDB; AA207228.  
XX  
PT Lung tumor specific polynucleotides for inhibiting the development of  
PT lung cancer.  
XX  
PS Example 6; Page 124-125; 171pp; English.  
XX  
CC The present invention describes lung tumour specific polynucleotides and  
CC tumour antigens. AA207144 to AA207246 and AA208301 to AA208325 represent  
CC specifically claimed polynucleotides, and AA29486 to AA29571 represent  
CC amino acid sequences from the present invention. The lung tumour specific  
CC polynucleotides and polypeptides can be used in pharmaceutical  
CC compositions and vaccines to inhibit the development of lung cancer. They  
CC can also be used to detect lung cancer in a patient. Probes and  
CC antibodies derived from the lung tumour sequences are useful in detection  
CC of lung cancer  
XX  
SQ Sequence 133 AA;  
Query Match 67.9%; Score 473; DB 2; Length 133;  
Best Local Similarity 70.3%; Pred. No. 6.9e-51;  
Matches 90; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

Best Local Similarity 70.3%; Pred. No. 6.9e-51;  
Matches 90; Conservative 14; Mismatches 24; Indels 0; Gaps 0;  
QY 1 MNHTSQAFITAAAGCGPPNYERIKEEYEVAEMGAPHGASVTRTTVINMPREVSVPDHVW 60  
DB 1 MNHTVQTFPVSNGQPPNYEMLKEEHEVAVLGAPHNPAPTSTVIHIRSTSVDPDHVW 60  
QY 61 SLFNTLFMNFCCGLGFIAYAYSVKSRDRKMVGDTVGAQAYASTAKCLNISTLVLSILMVVI 120  
DB 61 SLFNTLFMNFCCGLGFIAYAYSVKSRDRKMVGDTVGAQAYASTAKCLNIWALLILMITIL 120  
QY 121 TIVSVIII 128  
DB 121 LIVIPVLI 128  
RESULT 8  
ID AAB44456 standard; protein; 133 AA.  
XX  
AC AAB44456;  
XX  
DT 05-FEB-2001 (first entry)  
DE Human lung tumour-specific antigen encoded by cDNA #71.  
XX  
KW Lung tumour protein; lung cancer; cytostatic; vaccine.  
XX  
OS Homo sapiens.  
XX  
PN WO200060077-A2.  
XX  
PD 12-OCT-2000.  
XX  
PF 30-MAR-2000; 2000WO-US008560.  
XX  
PR 02-APR-1999; 99US-00285323.  
PR 09-AUG-1999; 99US-00370838.  
PR 30-DEC-1999; 99US-00476235.  
PR 03-MAR-2000; 2000US-00518809.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Reed SG, Lodes MJ, Mohamath R, Secretist H;  
XX  
DR WPI; 2000-638466/61.  
DR N-PSDB; AAC79118.  
XX  
PT Novel lung tumor polypeptides and polynucleotides, useful for detecting,  
PT monitoring or treating cancer, especially lung cancer.  
XX  
PS Claim 1; Page 140-141; 243pp; English.  
XX  
CC The present sequence is given in a specification relating to compounds  
CC for therapy and diagnosis of lung cancer. Polypeptides comprising at  
CC least an immunogenic part of a lung tumour protein are disclosed. The  
CC polypeptides are useful for inhibiting the development of cancer,  
CC especially lung cancer. Samples of T cells expressing the polypeptides  
CC may be used to inhibit the development of cancer. The polypeptides are  
CC also useful for detecting and monitoring the progression of cancer,  
CC especially lung cancer  
XX  
SQ Sequence 133 AA;  
Query Match 67.9%; Score 473; DB 3; Length 133;  
Best Local Similarity 70.3%; Pred. No. 6.9e-51;  
Matches 90; Conservative 14; Mismatches 24; Indels 0; Gaps 0;  
QY 1 MNHTSQAFITAAAGCGPPNYERIKEEYEVAEMGAPHGASVTRTTVINMPREVSVPDHVW 60  
DB 1 MNHTVQTFPVSNGQPPNYEMLKEEHEVAVLGAPHNPAPTSTVIHIRSTSVDPDHVW 60  
QY 61 SLFNTLFMNFCCGLGFIAYAYSVKSRDRKMVGDTVGAQAYASTAKCLNISTLVLSILMVVI 120

```
Db      61 SLFNTLFMNPCCGLGFIAPFAYSVKSRDRKMGVDVTGAQAYASTAKCLNIWALILGILMTIL 120
Qy      121 TIVSVIII 128
Db      121 LIVIPVLI 128

RESULT 9
AAE13797
ID AAE13797 standard; protein; 133 AA.
AC AAE13797;
XX
XX
XX 26-FEB-2002 (first entry)
DE
DE Human lung tumour-specific protein SALT-T8.
XX
XX Human; lung tumour protein; immunostimulant; cytostatic; gene therapy;
KW antitense-therapy; vaccine; immune response; lung cancer; SALT-T8.
XX
XX Homo sapiens.
OS
XX
XX WO200172295-A2.
XX
XX 04-OCT-2001.
XX
XX 28-MAR-2001; 2001WO-US0009991.
XX
XX 29-MAR-2000; 2000US-00538037.
XX
XX 05-JUN-2000; 2000US-00588937.
XX
XX 18-AUG-2000; 2000US-00640878.
XX
XX 22-SEP-2000; 2000US-0234517P.
XX
XX 01-NOV-2000; 2000US-00704512.
XX
XX 14-DEC-2000; 2000US-00738973.
XX
XX (CORI-) CORIXA CORP.
XX
XX Reed SG, Lodes MJ, Mohamath R, Secretist H, Benson DR, Indirias CV;
PI Henderson RA, Fling SP, Algate PA, Elliot M, Mannion J, Kalos WD;
XX
XX WPI; 2001-639201/73.
XX
XX N-PSDB; AAD23193.
XX
XX New human lung-specific polynucleotides and polypeptides for the
PT diagnosis and treatment of disease e.g. lung cancer.
XX
XX Example 6; Page 195; 378pp; English.
XX
XX The invention relates to isolated lung tumour-specific proteins and their
XX corresponding cDNA molecules. Lung tumour-specific proteins and their
XX antigen-presenting cells are useful for stimulating and/or expanding T
XX cells specific for a tumour protein, and for inhibiting the development
XX of cancer. The invention also relates to a composition useful for
XX stimulating an immune response, and for treating cancer. The lung tumour
XX specific oligonucleotide is useful in gene therapy and for diagnosis,
XX detection and treatment of lung cancer. The present sequence is human
XX lung tumour-specific protein
XX
XX Sequence 133 AA;

Query Match      67.9%; Score 473; DB 4; Length 133;
Best Local Similarity 70.3%; Pred. No. 6.9e-51;
Matches 90; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

Qy      1 MNHTSQAFITAAAGGQPPNVERIKEEYEAEMGAPHGASVRTTVINMPREVSVDPHVW 60
Db      1 MNHTVQTFPSVNSGQPPNVEMLKEEHEVAVLGAPHPAPTSTVTHIRSETSVDPHVW 60

Qy      61 SLFNTLFMNPCCGLGFIAPFAYSVKSRDRKMGVDVTGAQAYASTAKCLNIWALILGILMTIL 120
Db      61 SLFNTLFMNPCCGLGFIAPFAYSVKSRDRKMGVDVTGAQAYASTAKCLNIWALILGILMTIL 120
```

```
Qy      121 TIVSVIII 128
Db      121 LIVIPVLI 128

RESULT 10
ABR41053
ID ABR41053 standard; protein; 133 AA.
XX
XX ABR41053;
XX
XX 22-MAY-2003 (first entry)
DE
DE Human MAP kinase cascade activator #38.
XX
XX Human; Elk1 phosphorylation; Elk1 phosphorylation kinase; virucide;
KW antiinflammatory; immunomodulator; cytostatic; antiallergic; anti-HIV;
KW antirheumatic; antiarthritic; antidiabetic; antiasthmatic; gene therapy;
KW inflammation; autoimmune disease; viral disease; cancer; diabetes;
KW rheumatoid arthritis; asthma; allergic rhinitis; AIDS; viral hepatitis;
KW IgA nephritis.
XX
XX Homo sapiens.
OS
XX
XX WO2003008589-A1.
XX
XX 30-JAN-2003.
XX
XX 15-JUL-2002; 2002WO-JP007174.
XX
XX 18-JUL-2001; 2001JP-00218204.
XX
XX 31-AUG-2001; 2001JP-00263450.
XX
XX 21-JAN-2002; 2002JP-00012176.
XX
XX (ASAH ) ASAH KASEI KOGYO KK.
XX
XX Matsuzaki O, Matsuda A, Nagano Y, Suzuki N;
XX
XX WPI; 2003-229582/22.
XX
XX N-PSDB; ACC42319.
XX
XX Elk1 phosphorylation-associated gene and its encoded protein with MAP
PT kinase cascade effect, applicable in diagnosis of and developing drugs
PT for e.g. inflammations, autoimmune diseases, viral diseases and cancer.
XX
XX Claim 1; Page 290; 762pp; Japanese.
XX
XX The invention relates to a novel purified protein having Elk1
XX phosphorylation activity and/or an activity of activating Elk1
XX phosphorylation kinase. A protein of the invention has antiinflammatory,
XX immunomodulator, virucide, cytostatic, antiallergic, antirheumatic,
XX antiarthritic, antidiabetic, antiasthmatic, and anti-HIV activity. The
XX polynucleotides may have a use in gene therapy. The gene and its encoded
XX protein are applicable in diagnosis of and developing drugs for e.g.
XX inflammations, autoimmune diseases, viral diseases and cancer such as
XX rheumatoid arthritis, diabetes; asthma, allergic rhinitis, AIDS, viral
XX hepatitis and IgA nephritis. The present sequence is used in the
XX exemplification of the invention
XX
XX Sequence 133 AA;

Query Match      67.9%; Score 473; DB 6; Length 133;
Best Local Similarity 70.3%; Pred. No. 6.9e-51;
Matches 90; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

Qy      1 MNHTSQAFITAAAGGQPPNVERIKEEYEAEMGAPHGASVRTTVINMPREVSVDPHVW 60
Db      1 MNHTVQTFPSVNSGQPPNVEMLKEEHEVAVLGAPHPAPTSTVTHIRSETSVDPHVW 60

Qy      61 SLFNTLFMNPCCGLGFIAPFAYSVKSRDRKMGVDVTGAQAYASTAKCLNIWALILGILMTIL 120
Db      61 SLFNTLFMNPCCGLGFIAPFAYSVKSRDRKMGVDVTGAQAYASTAKCLNIWALILGILMTIL 120
```

QY 121 TIVSVIII 128  
DB 121 LIVIPVLI 128

RESULT 11  
ADD66432  
ID ADD66432 standard; protein; 133 AA.  
XX  
AC ADD66432;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human lung tumour-specific related protein, SEQ ID No 124.  
XX  
KW expression control; cancer; T cell; tumour; immune; cytostatic; vaccine;  
KW human; lung tumour-specific.  
XX  
OS Homo sapiens.  
XX  
PN WO200292001-A2.  
XX  
PD 21-NOV-2002.  
XX  
PF 10-MAY-2002; 2002WO-US014975.  
XX  
PR 11-MAY-2001; 2001US-00854133.  
XX  
PA (CORI-) CORIXA CORP.  
XX  
PI Lodes MJ, Wang T, Fan L, Algate PA, Mcneill PD;  
XX  
DR WPI; 2003-120592/11.  
XX  
PT New polynucleotide and polypeptide, useful for preparing a composition  
PT for diagnosing, treating or preventing cancer.  
XX  
PS Disclosure; SEQ ID NO 124; 494pp; English.  
XX  
CC The invention relates to a novel isolated polynucleotide comprising one  
CC of 32 47-6080 base pair sequences, given in the specification, or their  
CC complements or degenerate variants, at least 20 contiguous residues of a  
CC sequence in, or having at least 75 or 90 % identity with the isolated  
CC polynucleotide, or that hybridise with the polynucleotide. The invention  
CC further comprises: an isolated polypeptide; an expression vector  
CC comprising the polynucleotide operably linked to an expression control  
CC sequence; a host cell transformed or transfected with the expression  
CC vector; an isolated antibody or its antigen-binding fragment that  
CC specifically binds to the polypeptide; a method for detecting the  
CC presence of a cancer in a patient; a fusion protein comprising the  
CC polypeptide; an oligonucleotide that hybridises to the isolated  
CC polynucleotide under moderately stringent conditions; a method for  
CC stimulating and/or expanding T cells specific for a tumour protein; an  
CC isolated T cell population; a composition comprising a first component  
CC consisting of carriers and immunostimulants and a second component; a  
CC method for stimulating an immune response in a patient; a method for  
CC treating cancer in a patient; a method for determining cancer in a  
CC patient; a diagnostic kit comprising at least one oligonucleotide or  
CC antibody and a detection reagent comprising a reporter group; and a  
CC method for inhibiting the development of cancer in a patient. The  
CC compositions of the invention have cytostatic activity and can be used to  
CC create a vaccine. The isolated polynucleotide is useful for preparing a  
CC composition for diagnosing, treating or preventing cancer. This sequence  
CC represents a human lung tumour-specific protein relating to the  
CC invention.

Query Match 67.9%; Score 473; DB 7; Length 133;  
Best Local Similarity 70.3%; Pred. No. 6.9e-51;  
Matches 90; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 1 MNHTSQAFITAGGQPPNYERIKEEYEVAEMGAPHGSASVRTTINNPREVSVDPHVWV 60

DB 1 MNHTVQTFFSPVNSQPPNYEMLKEEHEVAVLGAPHNPAPTSTVIHIRSTSVDPHVWV 60

QY 61 SLFNTLFNFCCLGFIAYAYSVKSRDRKMGVDVTCGAQAYASTAKCLNISTLVLSILMVVI 120  
DB 61 SLFNTLFNFPCCCLGFIAYAYSVKSRDRKMGVDVTCGAQAYASTAKCLNISTLVLSILMVVI 120

QY 121 TIVSVIII 128  
DB 121 LIVIPVLI 128

RESULT 12  
ADE63839  
ID ADE63839 standard; protein; 133 AA.  
XX  
AC ADE63839;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human Protein Q01628, SEQ ID NO 9783.  
XX  
KW Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
OS Homo sapiens.  
XX  
PN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX  
DR WPI; 2003-268312/26.  
DR GENBANK; Q01628.  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
PS Claim 1; Page; 1017pp; English.  
XX  
CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene

CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 133 AA;

Query Match 67.9%; Score 473; DB 7; Length 133;  
Best Local Similarity 70.3%; Pred. No. 6.9e-51;  
Matches 90; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

Qy 1 MNHTSQAFITAAAGGQPPNYERIKEEYEVAEMGAPHGASVRTVTINMPREVSVDPHVW 60  
Db 1 MNHTVQTFSPVNGQPPNYEMLEKEHEVAVLGAPHNPAPTSTVIHIRSTSVDPHVW 60

Qy 61 SLFNTLFMNFCCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVVI 120  
Db 61 SLFNTLFMNFCCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNIWALILGILMTIL 120

Qy 121 TIVSVIII 128  
Db 121 LIVIPVLI 128

RESULT 14  
ADE87686  
ID ADE87686 standard; protein; 133 AA.  
XX  
AC ADE87686;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human lung tumour antigen polypeptide #50.  
XX  
KW Human; lung tumour antigen; cancer; lung cancer; CD4+; CD8+; T cell;  
KW immune response; immunostimulant; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN US2003118599-A1.  
XX  
PD 26-JUN-2003.  
XX  
PF 10-MAY-2002; 2002US-00144649.  
XX  
PR 02-APR-1999; 99US-00285323.  
PR 03-AUG-1999; 99US-00370838.  
PR 30-DEC-1999; 99US-00476235.  
PR 03-MAR-2000; 2000US-00518809.  
PR 29-MAR-2000; 2000US-00538037.  
PR 05-JUN-2000; 2000US-00588937.  
PR 18-AUG-2000; 2000US-00640878.  
PR 20-SEP-2000; 2000US-00667170.  
PR 01-NOV-2000; 2000US-00704512.  
PR 14-DEC-2000; 2000US-00738973.  
PR 11-MAY-2001; 2001US-00854133.  
XX  
PA (CORI-) CORIXA CORP.  
XX

CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 133 AA;

Query Match 67.9%; Score 473; DB 7; Length 133;  
Best Local Similarity 70.3%; Pred. No. 6.9e-51;  
Matches 90; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

Qy 1 MNHTSQAFITAAAGGQPPNYERIKEEYEVAEMGAPHGASVRTVTINMPREVSVDPHVW 60  
Db 1 MNHTVQTFSPVNGQPPNYEMLEKEHEVAVLGAPHNPAPTSTVIHIRSTSVDPHVW 60

Qy 61 SLFNTLFMNFCCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVVI 120  
Db 61 SLFNTLFMNFCCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNIWALILGILMTIL 120

Qy 121 TIVSVIII 128  
Db 121 LIVIPVLI 128

RESULT 13  
ADD46417  
ID ADD46417 standard; protein; 133 AA.  
XX  
AC ADD46417;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human Protein Q01628, SEQ ID NO 12097.  
XX  
KW Human; pain; neuronal tissue; Gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
OS Homo sapiens.  
XX  
PN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX  
WPI; 2003-269312/26.  
DR GENBANK; Q01628.  
XX  
PS New composition comprising two or more isolated polypeptides, useful for  
XX preparing a medicament for treating pain in an animal.  
XX  
PS Claim 1; Page; 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
CC human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal

PI Algate PA, Lodes MJ, Wang T, Fan L, McNeill PD;  
 XX WPI; 2003-897103/82.  
 DR N-PSDB; ADE87681.  
 XX  
 PT New polynucleotides encode lung tumor antigens and are useful to  
 PT stimulate an immune response or detect or treat a cancer in a patient,  
 PT particularly lung cancer.  
 XX  
 PS Example 6; SEQ ID NO 124; 63pp; English.  
 XX  
 CC The invention relates to polynucleotides encoding lung tumour antigens.  
 CC The invention also relates to the polypeptides encoded by the  
 CC polynucleotides, isolated antibodies or antigen-binding fragments that  
 CC specifically bind the polypeptides and a method for detecting cancer in a  
 CC patient, comprising obtaining a biological sample from the patient,  
 CC contacting the sample with a binding agent that binds a polypeptide of  
 CC the invention, detecting in the sample an amount of polypeptide that  
 CC binds to the binding agent, and comparing the amount of polypeptide to a  
 CC predetermined cut-off value. T cells specific for a tumour protein can be  
 CC stimulated and/or expanded by contacting the T cells with a polypeptide,  
 CC polynucleotide or an antigen-presenting cell that expresses a  
 CC polypeptide. Cancer development can be inhibited by incubating CD4+  
 CC and/or CD8+ T cells isolated from a patient with a polypeptide,  
 CC polynucleotide or an antigen-presenting cell that expresses a  
 CC polypeptide, so that the T cells proliferate. The invention is used to  
 CC stimulate an immune response or to detect or treat a cancer in a patient,  
 CC particularly lung cancer. This sequence represents a human lung tumour  
 CC antigen polypeptide of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification but was obtained in  
 CC electronic format from USPTO at seqdata.uspto.gov/sequence.html.  
 XX  
 SQ Sequence 133 AA;  
 Query Match 67.9%; Score 473; DB 7; Length 133;  
 Best Local Similarity 70.3%; Pred. No. 6.9e-51;  
 Matches 90; Conservative 14; Mismatches 24; Indels 0; Gaps 0;  
 QY 1 MNHTSQAFITAAAGCGPPNYERIKEEYEVAEMGAPHGASVRRVTVINMPREVSDPDHVVW 60  
 Db 1 MNHTVQTFFSPVNSGQPPNYEMLEKEHEVAVLGAPHPNPAPTSTVIHRSSTVSDPDHVVW 60  
 QY 61 SLFNTLFMNFCCGLFIAYAVSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSIMVVI 120  
 Db 61 SLFNTLFMNFCCGLFIAYAVSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSIMVVI 120  
 QY 121 TIVSVIII 128  
 Db 121 LIVIPVLI 128  
 RESULT 15  
 ABP43105  
 ID ABP43105 standard; protein; 143 AA.  
 XX  
 AC ABP43105;  
 XX  
 XX 22-AUG-2002 (first entry)  
 XX  
 DE Human ovarian antigen HVCBB19, SEQ ID NO:4237.  
 XX  
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;  
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;  
 KW inflammatory condition; immune disorder; blood disorder;  
 KW cardiovascular disorder; respiratory disorder; neurological disorder;  
 KW gastrointestinal disorder; urinary system disorder; drug screening;  
 KW gene therapy; chromosome mapping; forensic analysis;  
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
 KW antiinflammatory; gynaecological; reproductive.  
 XX  
 OS Homo sapiens.

XX WO200200677-A1.  
 XX  
 PD 03-JAN-2002.  
 XX  
 XX 07-JUN-2001; 2001WO-US018569.  
 PF  
 XX 07-JUN-2000; 2000US-0209467P.  
 PR  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Birse CE, Rosen CA;  
 PI  
 XX WPI; 2002-147878/19.  
 DR  
 XX N-PSDB; ABQ56182.  
 XX  
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,  
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian  
 PT cancer), immune disorders, cardiovascular disorders and neurological  
 PT diseases.  
 XX  
 PS Claim 11; SEQ ID NO 4237; 2922pp; English.  
 XX  
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-  
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also  
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical  
 CC to the sequences of the invention. The invention additionally relates to  
 CC recombinant vectors and host cells comprising human ovarian antigen  
 CC polynucleotides, antibodies against human ovarian antigens, and the use  
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,  
 CC treating, prognosing or preventing various ovary and/or breast-related  
 CC disorders. Such conditions include ovarian cancer and breast cancer, and  
 CC metastatic tumours of ovarian or breast origin, reproductive system  
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,  
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine  
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic  
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and  
 CC vaginitis), immune disorders (e.g., congenital and acquired  
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),  
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,  
 CC respiratory disorders, neurological disorders, gastrointestinal disorders  
 CC and urinary system disorders. Ovarian antigen polypeptides and  
 CC polynucleotides may also be used in screening for compounds which  
 CC modulate ovarian antigen expression or activity. The polynucleotides may  
 CC further be used for gene therapy, chromosome mapping, in the  
 CC identification of individuals and in forensic analysis, and the  
 CC polypeptides may be used as food additives or to prepare antibodies  
 CC useful in disease diagnosis, drug targeting and phenotyping. The present  
 CC sequence represents a human ovarian antigen of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 143 AA;  
 Query Match 67.9%; Score 473; DB 5; Length 143;  
 Best Local Similarity 70.3%; Pred. No. 7.6e-51;  
 Matches 90; Conservative 14; Mismatches 24; Indels 0; Gaps 0;  
 QY 1 MNHTSQAFITAAAGCGPPNYERIKEEYEVAEMGAPHGASVRRVTVINMPREVSDPDHVVW 60  
 Db 11 MNHTVQTFFSPVNSGQPPNYEMLEKEHEVAVLGAPHPNPAPTSTVIHRSSTVSDPDHVVW 70  
 QY 61 SLFNTLFMNFCCGLFIAYAVSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSIMVVI 120  
 Db 71 SLFNTLFMNFCCGLFIAYAVSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSIMVVI 130  
 QY 121 TIVSVIII 128  
 Db 131 LIVIPVLI 138  
 Search completed: June 18, 2005, 16:31:42

Job time : 164 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2005, 16:17:44 ; Search time 177 Seconds  
(without alignments)  
396.355 Million cell updates/sec

Title: US-10-621-911A-2  
Perfect score: 697  
Sequence: 1 MNHRSQAFITRAGGQPPNY.....VVITIVSVIIIVLNAQNLT 137

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03.\*  
1: uniprot\_eprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID           | Description         |
|------------|-------|-------------|--------|--------------|---------------------|
| 1          | 697   | 100.0       | 137    | Q9CQW9       | Q9CQW9 m mus muscu  |
| 2          | 693   | 99.4        | 137    | Q9D8L6       | Q9D8L6 mus musculus |
| 3          | 646   | 92.7        | 137    | INIB RAT     | P26376 rattus norv  |
| 4          | 497.5 | 71.4        | 144    | Q9R175       | Q9R175 rattus norv  |
| 5          | 497   | 71.3        | 144    | Q9S793       | Q9S793 mus musculus |
| 6          | 473   | 67.9        | 133    | 1 IFN3_HUMAN | Q01628 homo sapien  |
| 7          | 454   | 65.1        | 132    | Q6F8H2       | Q6F8H2 homo sapien  |
| 8          | 452   | 64.8        | 146    | Q9SMQ3       | Q9SMQ3 bos taurus   |
| 9          | 449   | 64.4        | 132    | 1 IFM2_HUMAN | Q01629 homo sapien  |
| 10         | 427   | 61.3        | 93     | Q9R176       | Q9R176 rattus norv  |
| 11         | 388.5 | 55.7        | 107    | Q9D3R8       | Q9D3R8 mus musculus |
| 12         | 388.5 | 55.7        | 113    | Q8BVR2       | Q8BVR2 mus musculus |
| 13         | 385.5 | 55.3        | 106    | Q9D103       | Q9D103 mus musculus |
| 14         | 385.5 | 55.3        | 106    | Q8R2S7       | Q8R2S7 mus musculus |
| 15         | 384.5 | 55.2        | 125    | 1 IFM1_HUMAN | P13164 homo sapien  |
| 16         | 378.5 | 54.3        | 125    | Q9SMQ2       | Q9SMQ2 bos taurus   |
| 17         | 268.5 | 38.5        | 152    | Q7S7S1       | Q7S7S1 xenopus lae  |
| 18         | 266   | 38.2        | 152    | Q14617       | Q14617 homo sapien  |
| 19         | 225   | 32.3        | 107    | 1 I14K_TORMA | Q91499 torpedo mar  |
| 20         | 210   | 30.1        | 128    | Q8QFL3       | Q8QFL3 oncorhynch   |
| 21         | 203   | 29.1        | 127    | Q8QFM4       | Q8QFM4 oncorhynch   |
| 22         | 194.5 | 27.9        | 130    | Q810P6       | Q810P6 mus musculus |
| 23         | 191.5 | 27.5        | 134    | Q88728       | Q88728 mus musculus |
| 24         | 155.5 | 22.3        | 92     | Q88UH1       | Q88UH1 ictalurus p  |
| 25         | 129.5 | 18.6        | 162    | Q8BR26       | Q8BR26 mus musculus |
| 26         | 109.5 | 15.7        | 340    | Q96FA8       | Q96FA8 homo sapien  |
| 27         | 109.5 | 15.7        | 340    | Q7Z6L0       | Q7Z6L0 homo sapien  |
| 28         | 109.5 | 15.7        | 394    | Q8N2N8       | Q8N2N8 homo sapien  |
| 29         | 108   | 15.5        | 341    | Q8ND36       | Q8ND36 homo sapien  |
| 30         | 100.5 | 14.4        | 111    | Q8PQ26       | Q8PQ26 xanthomonas  |
| 31         | 96.5  | 13.8        | 114    | Q8PD53       | Q8PD53 xanthomonas  |

|    |      |      |     |   |            |                     |
|----|------|------|-----|---|------------|---------------------|
| 32 | 96   | 13.8 | 179 | 2 | Q6DFT4     | Q6DFT4 xenopus tro  |
| 33 | 86.5 | 12.4 | 169 | 2 | Q9NC83     | Q9NC83 strongyloce  |
| 34 | 83.5 | 12.0 | 688 | 2 | Q950Y4     | Q950Y4 tetrahymena  |
| 35 | 83.5 | 12.0 | 688 | 2 | Q9T7M6     | Q9T7M6 tetrahymena  |
| 36 | 83.5 | 12.0 | 698 | 1 | COX1_TETPY | P11947 tetrahymena  |
| 37 | 83   | 11.9 | 173 | 2 | Q8C838     | Q8C838 mus musculus |
| 38 | 83   | 11.9 | 722 | 2 | Q8Y3Q8     | Q8Y3Q8 listeria mo  |
| 39 | 82.5 | 11.8 | 722 | 2 | Q71VY5     | Q71VY5 listeria mo  |
| 40 | 80   | 11.5 | 110 | 2 | Q73T16     | Q73T16 mycobacteri  |
| 41 | 80   | 11.5 | 645 | 1 | COX1_PARTB | P05489 paramecium   |
| 42 | 79.5 | 11.4 | 257 | 2 | Q8H0E2     | Q8H0E2 schizosacch  |
| 43 | 78   | 11.2 | 258 | 1 | CT39_HUMAN | Q9H7V2 homo sapien  |
| 44 | 78   | 11.2 | 324 | 2 | Q67ER8     | Q67ER8 rattus norv  |
| 45 | 77.5 | 11.1 | 254 | 2 | Q88Y29     | Q88Y29 lactobacilli |

ALIGNMENTS

RESULT 1  
Q9CQW9 PRELIMINARY; PRT; 137 AA.  
AC Q9CQW9;  
DT 01-JUN-2001 (TREMELrel. 17, Created)  
DT 25-OCT-2004 (TREMELrel. 28, Last sequence update)  
DE Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched  
DE library, clone:1810061A10 product:INTERFERON-INDUCIBLE PROTEIN homolog  
DE (Mus musculus 18-day embryo whole body cDNA, RIKEN full-length  
DE enriched library, clone:111004C05 product:INTERFERON-INDUCIBLE  
DE PROTEIN homolog) (Fragilis) (interferon-inducible protein 15)  
DE (Interferon induced transmembrane protein 3).  
GS Name=Ifitm3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
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EX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning."  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
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RC STRAIN=C57BL/6J; TISSUE=Pancreas, and Whole body;  
EX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
RN [3]  
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EX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
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RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
RN [4]  
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RL Nature 409:685-690(2001).  
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RL Nature 409:685-690(2001).  
RN [6]  
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RL Nature 409:685-690(2001).  
RN [7]  
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RN [8]  
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RL Nature 409:685-690(2001).  
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RN [13]  
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EX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection."  
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RC STRAIN=FVB/N-3; TISSUE=Mammary tumor;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
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DR EMBL; AK007919; BAB25350.1; -;  
DR EMBL; AK003407; BAB22771.1; -;  
DR EMBL; AY082484; AAW03316.1; -;

DR EMBL; AV594690; AAT06089.1; -;  
DR EMBL; BC010291; AAR10291.1; -;  
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DR GO; GO:0016023; C:cytoplasmic vesicle; IDA.  
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Db |||||  
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DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
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RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
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RT "Functional annotation of a full-length mouse cDNA collection.",  
RL Nature 409:685-690(2001).  
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RL Nature 409:685-690(2001).  
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RL Nature 409:685-690(2001).  
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RL Nature 409:685-690(2001).  
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RL Nature 409:685-690(2001).  
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RL Nature 409:685-690(2001).  
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RL Nature 409:685-690(2001).  
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RL Nature 409:685-690(2001).  
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RT "Functional annotation of a full-length mouse cDNA collection.",  
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RT "Functional annotation of a full-length mouse cDNA collection.",  
RL Nature 409:685-690(2001).  
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RT "Functional annotation of a full-length mouse cDNA collection.",  
RL Nature 409:

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RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kikunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771 (2000).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK007916; BAB25347.1; -.
DR MGD; MGI:1913391; Ifitm3.
DR GO; GO:0016023; C:cytoplasmic vesicle; IDA.
DR GO; GO:0008285; P:negative regulation of cell proliferation; IDA.
DR InterPro; IPR007593; CD225.
DR Pfam; PF04505; CD225; 1
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QY 1 MNHTSQAFITAAAGCGPPNYERIKEEYEVAEMGAPHGASVRTTINNPREVSVDPHVW 60
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DB 121 TIVSVIIIVLNAQNLT 137

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DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interferon-inducible protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
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RA Hayzer D.J.;
RL Submitted (AUG-1991) to the EMBL/GenBank/DBJ databases.
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CC -!- INDUCTION: By interferon beta.
CC -!- SIMILARITY: Belongs to the IFN-induced transmembrane protein

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CC family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X61381; CAA43655.1; -.
DR InterPro; IPR007593; CD225.
DR Pfam; PF04505; CD225; 1.
KW Interferon induction; Transmembrane.
FT TRANSMEM 58 78 Potential.
FT TRANSMEM 110 130 Potential.
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DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interferon-inducible protein 16 (Hypothetical protein).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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RX MEDLINE=22531601; PubMed=12644301; DOI=10.1016/S0303-7207(02)00412-4;
RA Daido H., Zhou M.Y., Gomez-Sanchez E.P., Gomez-Sanchez C.E.;
RT "Interferon-inducible genes in the rat adrenal gland and vascular
RL smooth muscle cells."
RL Mol. Cell. Endocrinol. 200:81-87 (2003).
RN [2]
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RC TISSUE=Pituitary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

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RA Kzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary gland;
RA Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF164040; AAB48011.1; -.
DR EMBL; BC060563; AAB60563.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009607; P:response to biotic stimulus; IEA.
DR InterPro; IPR007593; CD225.
DR Pfam; PF04505; CD225; 1.
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DB 120 CIIIFSTTSVAVFOSLSORTPHS 142
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DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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DE R).
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvEv;
RA Saitou M., Barton S., Surani M.A.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002160; AAB02160.1; -.
DR EMBL; BC002102; AAB02102.1; -.
DR EMBL; AY082486; AAM03318.1; -.
DR MGD; MGI:1933382; Ifitm2.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR007593; CD225.
DR Pfam; PF04505; CD225; 1.
KW Transmembrane.
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DB 1 MSHNSQAFI-L-STNAGLPSPVETIKEEYGVTELGPNSAVVRTTINNPREVSPDHHVW 59
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DB 120 CIIIFSTTSVAVFQSPAQ 137
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DT 01-JUL-1993 (Rel. 26, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUN-2004 (Rel. 41, Last annotation update)
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DE protein 1-8U).
GN Name=IFITM3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91301153; PubMed=1906403;
RA Lewin A.R., Reid L.E., McMahon M., Stark G.R., Kerr I.M.;
RT "Molecular analysis of a human interferon-inducible gene family.";
RL Eur. J. Biochem. 199:417-423(1991).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Cervix;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -!- INDUCTION: By alpha and gamma interferons.  
CC -!- SIMILARITY: Belongs to the IFN-induced transmembrane protein  
CC family.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; X57352; CAA40626.1; -;  
DR EMBL; BC006794; AAH06794.1; -;  
DR EMBL; BC008417; AAH08417.1; -;  
DR EMBL; BC022439; AAH22439.1; -;  
DR PIR; S17182; S17182.  
DR Genew; HGNC:5414; IFITM3.  
DR H-InvDB; HIX0021368; -;  
DR MIM; 605579; -;  
DR GO; GO:0006955; P:immune response; TAS.  
DR InterPro; IPR007593; CD225.  
DR Pfam; PF04505; CD225; 1.  
KW Interferon induction; Transmembrane.  
FT TRANSMEM 58 78 Potential.  
FT TRANSMEM 108 128 Potential.  
FT CONFLICT 2 2 N -> S (in Ref. 1).  
FT CONFLICT 3 3 H -> Q (in Ref. 2; AAH08417/AAH22439).  
FT CONFLICT 34 34 A -> G (in Ref. 1).  
SQ SEQUENCE 133 AA; 14632 MW; 9FFB2B4623F7A1DD CRC64;  
Query Match 67.9%; Score 473; DB 1; Length 133;  
Best Local Similarity 70.3%; Pred. No. 1.2e-41;  
Matches 90; Conservative 14; Mismatches 24; Indels 0; Gaps 0;  
QY 1 MNHTSQAFITTAASGGQPPNYERIKEEYEVAEMGAPHGASVTRTTVINMPREVSVPDHYVW 60  
DB 1 MNHTVQTFSPVNSGQPPNYEMLKEEHEVAVLGAPHPAPPTSTVIHRSSTVSDPDHYVW 60  
QY 61 SLFNTLFNMFCCGLFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSTLMVVI 120  
DB 61 SLFNTLFNMFCCGLFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSTLMVVI 120  
QY 121 TIVSVIII 128  
DB 121 LIVPVLII 128  
RESULT 7  
Q6FH82 PRELIMINARY; PRT; 132 AA.  
AC Q6FH82;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE IFITM2 protein (Fragment).  
GN Name=IFITM2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Halleck A., Ebert L., Mkundinya M., Schick M., Eisenstein S.,  
RA Neubert P., Ketrang K., Schatten R., Shen B., Henze S., Mar W.,  
RA Korn B., Zuo D., Hu Y., Labaer J.,  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CR541874; CAG46672.1; -;  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR InterPro; IPR007593; CD225.  
DR Pfam; PF04505; CD225; 1.  
FT NON\_TER 132 132  
SQ SEQUENCE 132 AA; 14604 MW; 2B9B09CF7E05FB3 CRC64;  
Query Match 65.1%; Score 454; DB 2; Length 132;  
Best Local Similarity 66.9%; Pred. No. 1.2e-39;  
Matches 89; Conservative 16; Mismatches 26; Indels 2; Gaps 2;  
QY 1 MNHTSQAFITTAASGGQPPNYERIKEEYEVAEMGAPHGASVTRTTVINMPREVSVPDHYVW 60  
DB 1 MNHIVQTF-SPVNSGQPPNYEMLKEEHEVAVLGAPHPAPPTSTVIHRSSTVSDPDHYVW 59  
QY 61 SLFNTLFNMFCCGLFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSTLMVVI 120  
DB 60 SLFNTLFNMFCCGLFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSTLMVVI 119  
QY 121 TIVSVIII 133  
DB 120 LII-IPVLVQAQ 131  
RESULT 8  
Q95MQ3 PRELIMINARY; PRT; 146 AA.  
AC Q95MQ3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Interferon-induced protein 1-8U.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21526490; PubMed=11673264;  
RA Pru J.K., Austin K.J., Haas A.L., Hansen T.R.;  
RT "Pregnancy and interferon-tau upregulate gene expression of members of  
RT the 1-8 family in the bovine uterus.";  
RL Biol. Reprod. 65:1471-1480 (2001).  
DR EMBL; AF272041; AAK58638.1; -;  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR InterPro; IPR007593; CD225.  
DR Pfam; PF04505; CD225; 1.  
SQ SEQUENCE 146 AA; 15723 MW; E8A6FC3E5A7FB19D CRC64;  
Query Match 64.8%; Score 452; DB 2; Length 146;  
Best Local Similarity 67.2%; Pred. No. 2.1e-39;  
Matches 84; Conservative 18; Mismatches 23; Indels 0; Gaps 0;  
QY 1 MNHTSQAFITTAASGGQPPNYERIKEEYEVAEMGAPHGASVTRTTVINMPREVSVPDHYVW 60  
DB 1 MNRTSQLLLTGAGVAPPPAYEVLKEEHEVAVLGAPQAPLTTTINIRSDTAVPDHYVW 60  
QY 61 SLFNTLFNMFCCGLFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSTLMVVI 120  
DB 61 SLFNTLFNMFCCGLFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSTLMVVI 120  
QY 121 TIVSV 125  
DB 121 LIVLV 125

```
RESULT 9
IFM2 HUMAN
ID IFM2 HUMAN STANDARD; PRT; 132 AA.
AC Q01629; Q96DA8;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon-induced transmembrane protein 2 (Interferon-inducible
DE protein 1-8D).
GN Name=IFITM2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=91301153; PubMed=1906403;
RA Lewin A.R., Reid L.E., McMahon M., Stark G.R., Kerr I.M.;
RT "Molecular analysis of a human interferon-inducible gene family.";
RL Eur. J. Biochem. 199;417-423(1991).
RN [2]
SEQUENCE FROM N.A.
RP TTSUB=Lung;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Shat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.F., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullaby S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99;16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- INDUCTION: By alpha and gamma interferons.
CC -!- SIMILARITY: Belongs to the IFN-induced transmembrane protein
CC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X57351; CAA0625.1; -.
CC EMBL; BC009696; AAH09696.1; -.
CC PIR; S17183; S17183.
CC Genew; HGNC:5413; IFITM2.
CC MIM; 605578; -.
CC GO; GO:0006955; P:immune response; TAS.
CC InterPro; IPR007593; CD225.
CC Pfam; PF04505; CD225; 1.
CC Interferon induction; Polymorphism; Transmembrane.
FT TRANSMEM 57 77 Potential.
FT VARIANT 41 41 T -> M (in dbSNP:14408).
FT 41 41 G -> A (in Ref. 2).
FT CONFLICT 33 33
FT SEQUENCE 132 AA; 14546 MW; D42F47CA225D3465 CRC64;
SQ
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Query Match 64.4%; Score 449; DB 1; Length 132;
Best Local Similarity 65.4%; Pred. No. 3.9e-39;
Matches 87; Conservative 17; Mismatches 27; Indels 2; Gaps 2;

QY 1 MNHTSQAFITAAASGGOPPNYERIKEEYVAEMGAPHSASVRTTVINMPREVSVPDHVW 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 1 MNHIVQTF-SPVNSGQPPNYEMLEKEQEVAMLGPPHPAPPTSTVIHIRSTVDPDHVW 59
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 61 SLENTLFMNFCCILGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLINISLVLMMVI 120
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 60 SLENTLFMNTCCILGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLINIALILGFWTIL 119
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 121 TIVSVIIIVLNAQ 133
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 120 LVI-IPVLVVQAQ 131
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 10
Q9RL176 PRELIMINARY; PRT; 93 AA.
AC Q9RL176;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Interferon-inducible protein variant 10.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=22531601; PubMed=12644301; DOI=10.1016/S0303-7207(02)00412-4;
RA Daido H., Zhou M.Y., Gomez-Sanchez E.P., Gomez-Sanchez C.E.;
RT "Interferon-inducible genes in the rat adrenal gland and vascular
RT smooth muscle cells.";
RL Mol. Cell. Endocrinol. 200;81-87(2003).
DR EMBL; AF164039; AAD48010.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009607; P:response to biotic stimulus; IEA.
DR InterPro; IPR007593; CD225.
DR Pfam; PF04505; CD225; 1.
SQ SEQUENCE 93 AA; 10241 MW; 98130648468A9215 CRC64;

Query Match 61.3%; Score 427; DB 2; Length 93;
Best Local Similarity 94.0%; Pred. No. 5.5e-37;
Matches 78; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNHTSQAFITAAASGGOPPNYERIKEEYVAEMGAPHSASVRTTVINMPREVSVPDHVW 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 1 MNHTSQAFVNAATGGQPPNYERIKEEYVSELGAPHSASVRTTVINMPREVSVPDHVW 60
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

QY 61 SLENTLFMNFCCILGFIAYAYSVK 83
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
DB 61 SLENTLFMNFCCILGFIAYAYSVK 83
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 11
Q9D3R8 PRELIMINARY; PRT; 107 AA.
AC Q9D3R8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4933438K12 product:similar to INTERFERON-INDUCIBLE
DE PROTEIN.
GN Name=ifitm7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP
```



|                   |   |   |         |
|-------------------|---|---|---------|
| Qy                | 84  | SRRDKNVGDVTGAQAAYASTAKCLNISTIVLSILMWITI | 122     |
| Dd                | 62  | SRRDKNVGDMTGAQAFASTARCLNISCLISVVWVLPI   | 100     |
| RESULT 12         |   |   |         |
| Q8BVR2            | PRELIMINARY;  | PRT;                                    | 113 AA. |
| ID                | Q8BVR2;   |   |         |
| DC                | Q8BVR2;   |   |         |
| DT                | 01-MAR-2003 (TREMBLrel. 23, Created)  |   |         |
| DT                | 01-MAR-2003 (TREMBLrel. 23, Last sequence update)   |   |         |
| DT                | 01-JUN-2003 (TREMBLrel. 24, Last annotation update)   |   |         |
| DE                | Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:493057H06 product:similar to INTERPERON-INDUCIBLE PROTEIN. |   |         |
| DE                | MUS   |   |         |
| OS                | Mus musculus (Mouse).   |   |         |
| OC                | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;   |   |         |
| OX                | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.  |   |         |
| NCBI_TaxID=10090; | [1]   |   |         |
| RN                | SEQUENCE FROM N.A.  |   |         |
| RN                | STRAIN=C57BL/6J; TISSUE=Testis;   |   |         |
| RC                | MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;   |   |         |
| RX                | Carninci P., Hayashizaki Y.;  |   |         |
| RA                | "High-efficiency full-length cDNA cloning.";  |   |         |
| RL                | Meth. Enzymol. 303:19-44(1999).   |   |         |
| RN                | [2]   |   |         |
| RN                | SEQUENCE FROM N.A.  |   |         |
| RP                | STRAIN=C57BL/6J; TISSUE=Testis;   |   |         |
| RC                | MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  |   |         |
| RX                | RIKEN FANTOM Consortium;  |   |         |
| RA                | "Functional annotation of a full-length mouse cDNA collection.";  |   |         |
| RL                | Nature 409:685-690(2001).   |   |         |
| RN                | [3]   |   |         |
| RN                | SEQUENCE FROM N.A.  |   |         |
| RP                | STRAIN=C57BL/6J; TISSUE=Testis;   |   |         |
| RC                | STRAIN=C57BL/6J; TISSUE=Testis;   |   |         |
| RA                | The FANTOM Consortium,  |   |         |
| RA                | the RIKEN Genome Exploration Research Group Phase I & II Team;  |   |         |
| RA                | "Analysis of the mouse transcriptome based on functional annotation of  |   |         |
| RT                | 60,770 full-length cDNAs.";   |   |         |
| RT                | Nature 420:563-573 (2002).  |   |         |
| RN                | [4]   |   |         |
| RN                | SEQUENCE FROM N.A.  |   |         |
| RP                | STRAIN=C57BL/6J; TISSUE=Testis;   |   |         |
| RC                | MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;   |   |         |
| RX                | Carninci P., Shibata K., Hayatsu N., Suganara Y., Shibata K., Itoh M.,  |   |         |
| RA                | Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;   |   |         |
| RT                | "Normalization and subtraction of cap-trapper-selected cDNAs to   |   |         |
| RT                | prepare full-length cDNA libraries for rapid discovery of new genes."   |   |         |
| RT                | Genome Res. 10:1617-1630(2000).   |   |         |
| RN                | [5]   |   |         |
| RN                | SEQUENCE FROM N.A.  |   |         |
| RP                | STRAIN=C57BL/6J; TISSUE=Testis;   |   |         |
| RC                | MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;   |   |         |
| RX                | Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,   |   |         |
| RA                | Konno H., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M.,   |   |         |
| RA                | Sumi N., Ishii Y., Nakamura S., Hagihara M., Hashiguchi T., Harada A.,  |   |         |
| RA                | Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  |   |         |
| RA                | Fujikake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,  |   |         |
| RA                | Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  |   |         |
| RA                | Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  |   |         |
| RT                | "RIKEN integrated sequence analysis (RISA) system-384-format  |   |         |
| RT                | sequencing pipeline with 384 multicapillary sequencer.";  |   |         |
| RT                | Genome Res. 10:1757-1771(2000).   |   |         |
| RN                | [6]   |   |         |
| RN                | SEQUENCE FROM N.A.  |   |         |
| RP                | STRAIN=C57BL/6J; TISSUE=Testis;   |   |         |
| RC                | Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,   |   |         |
| RA                | Fukuda S., Furuno M., Hangaki T., Hara A., Hashizume W.,  |   |         |
| RA                | Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,   |   |         |
| RA                | Hori F., Imokita K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,   |   |         |
| RA                | Katoh H., Kawai J., Kotima Y., Kondo S., Konno H., Kouda M., Koya S.,   |   |         |

|     |  |
|-----|--|
| 16] | SEQUENCE FROM N.A.   |
| RP  | STRAIN-C57BL/6J; TISSUE-Testis;                                      |
| RC  | Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  |
| RC  | Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,             |
| RA  | Fukaya S., Furuno M., Hanagaki T., Hiraoka T., Hirozane T.,          |
| RA  | Fuyashida K., Hayatsu N., Hiramoto K., Hiraoka T., Kasukawa T.,      |
| RA  | Hori F., Imokani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,      |
| RA  | Kato H., Kawai J., Kotima Y., Kondo S., Konno H., Kouda M., Koya S., |
| RA  | Kato H., Kawai J., Kotima Y., Kondo S., Konno H., Kouda M., Koya S., |

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RA Kurihara C., Mateuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK076846; C36505.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009607; P:response to biotic stimulus; IEA.
DR InterPro; IPR007593; CD225.
DR Pfam; PF04505; CD225; 1.
SQ SEQUENCE 113 AA; 12679 MW; A016A02PB57B3310 CRC64;

Query Match 55.7%; Score 388.5; DB 2; Length 113;
Best Local Similarity 73.7%; Pred. No. 7.6e-33;
Matches 73; Conservative 14; Mismatches 11; Indels 1; Gaps 1;

QY 24 KEEYEVAEMGAPHGASASVRTTVMNPREVSPDHVWVSLFNTLPMNFCCLGFTAYAYSVK 83
DB 3 KQHEVVVMTGPHSTSTTTIITMP-EISKPDVWVWVSLFNTLPMNFCCLGFTAYAYSVK 61

QY 84 SRDRKMWGDTGTAQAYASTAKCLNISTLVLSILMVITV 122
DB 62 SRDRKMWGDTGTAQAFASATACLNISCLISLVWVILFI 100

RESULT 13
Q9D103 PRELIMINARY; PRT; 106 AA.
AC Q9D103;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched
DE library, clone:110036C17 product:similar to INTERFERON-INDUCIBLE
DE PROTEIN (Fragilis2).
GN Name=Ifitm1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
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[5]
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Oyeda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahita S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RN SEQUENCE FROM N.A.
RP MEDLINE=22944754; PubMed=12659663; DOI=10.1186/1471-213X-3-1;
RX Lange U., Saitou M., Western P., Barton S., Surani M.;
RT "The fragilis interferon-inducible gene family of transmembrane
RT proteins is associated with germ cell specification in mice.";
RL BMC Dev. Biol. 3:1-1(2003).
RN [8]
RN SEQUENCE FROM N.A.
RP Lange U.C., Saitou M., Surani M.A.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK004121; BAB23181.1; -.
DR EMBL; BK001123; DAA01238.1; -.
DR MGD; MGI:1915963; Ifitm1.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR007593; CD225.
DR Pfam; PF04505; CD225; 1.
SQ SEQUENCE 106 AA; 11524 MW; 7B0E7D8200D36631 CRC64;

Query Match 55.3%; Score 385.5; DB 2; Length 106;
Best Local Similarity 73.0%; Pred. No. 1.5e-32;
Matches 73; Conservative 10; Mismatches 16; Indels 1; Gaps 1;

QY 24 KEEYEVAEMGAPHGASASVRTTVMNPREVSPDHVWVSLFNTLPMNFCCLGFTAYAYSVK 83
DB 3 KEEQEVVVLGSPHISTATATTINMP-EISTPDHVWVSLFNTLPMNFCCLGFTAYAYSVK 61

QY 84 SRDRKMWGDTGTAQAYASTAKCLNISTLVLSILMVITV 123
DB 62 SRDRKMWGDTTGAQAFASATACLNISLFTILTAVIV 101

RESULT 14
Q8R2S7 PRELIMINARY; PRT; 106 AA.
AC Q8R2S7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interferon induced transmembrane protein 1.
GN Name=Ifitm1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Query Match 55.2%; Score 384.5; DB 1; Length 125;  
Best Local Similarity 67.3%; Pred. No. 2.2e-32;  
Matches 76; Conservative 16; Mismatches 18; Indels 3; Gaps 1;

Query Match 55.2%; Score 384.5; DB 1; Length 125;  
Best Local Similarity 67.3%; Pred. No. 2.2e-32;  
Matches 76; Conservative 16; Mismatches 18; Indels 3; Gaps 1;

Qy 24 KEEYEVAEMGAPHSASVRTVINMPREVSVPDHHVWSLENTLFMAFCCCLGFIAYAYSVK 83  
Db 3 KEEHEVAVLGAPPSTILPRSTVINIHSETSVDPDHHVWSLENTLFMAWCCCLGFIAYAYSVK 62  
Qy 84 SRDRKMWGDVTGAQAYASTAKCLNISTVLISILMWITIVSVIIIVLNAQNLH 136  
Db 63 SRDRKMWGDVTGAQAYASTAKCLNINWALILGILM---TIGFILLVFGSVTVY 112

Search completed: June 18, 2005, 16:34:45  
Job time : 180 secs